

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2005, 09:47:53 ; Search time 30.4577 Seconds
(without alignments)
882.327 Million cell updates/sec

Title: US-09-830-972-2-FUSED
Perfect score: 1823
Sequence: 1 MEDIDQSSLVSSSTDSPPRP.....VKDAMAKIOAKIPLKRRAD 360

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.1

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	904	49.6	199	2	US-08-700-607-1
2	904	49.6	201	4	US-09-949-016-9124
3	826.3	45.3	776	2	US-08-700-607-5
4	826.3	45.3	776	4	US-09-949-016-6998
5	816.7	44.8	439	4	US-09-949-016-9180
6	790	43.3	356	2	US-08-700-607-6
7	683	37.5	208	2	US-08-700-607-7
8	669	36.7	267	2	US-08-700-607-8
9	625.9	34.3	192	4	US-09-949-016-8859
10	585.3	32.1	588	4	US-09-949-016-7290
11	548.1	30.1	241	2	US-08-700-607-3
12	539.9	29.6	168	4	US-09-149-476-563
13	522	28.6	219	4	US-09-270-767-45132
14	286.8	15.7	68	4	US-09-513-999C-6304
15	286	15.7	92	4	US-09-149-476-411
16	262.8	14.4	1027	4	US-09-902-540-11750
17	262.5	14.4	75	4	US-09-621-976-4600
18	262.5	14.4	75	4	US-09-621-976-4601
19	253.2	13.9	1255	2	US-09-080-897-4
20	253.2	13.9	1255	3	US-08-899-595-1
21	252.5	13.9	1255	3	US-09-323-735-4
22	252.5	13.9	1248	2	US-09-080-897-2
23	252.5	13.9	1248	3	US-09-323-735-2
24	250	13.7	114	4	US-09-513-999C-7861
25	248.8	13.6	1315	3	US-08-899-595-3
26	241.5	13.2	744	4	US-09-902-540-15347
27	240.6	13.2	990	4	US-09-949-016-10562

28	238.5	13.1	1318	4	US-10-237-551-197	Sequence 197, Appl
29	236.6	13.0	933	3	US-08-764-870-14	Sequence 14, Appl
30	236.6	13.0	933	3	US-08-980-115-14	Sequence 14, Appl
31	236.3	13.0	2142	4	US-09-538-092-1142	Sequence 1142, Ap
32	236.2	13.0	1326	4	US-09-688-188B-15	Sequence 15, Appl
33	236.2	13.0	1326	4	US-09-291-417D-15	Sequence 15, Appl
34	235.7	12.9	8991	4	US-08-714-741-32	Sequence 32, Appl
35	235.1	12.9	1290	4	US-09-248-796A-20654	Sequence 20654, A
36	230.6	12.6	1560	4	US-09-264-512B-2	Sequence 2, Appli
37	230.4	12.6	1341	4	US-09-949-016-6890	Sequence 6890, Ap
38	230.4	12.6	1344	4	US-09-949-016-10925	Sequence 10925, A
39	228.8	12.6	1070	3	US-08-922-635-22	Sequence 22, Appl
40	228.8	12.6	1504	4	US-09-364-206-2	Sequence 2, Appli
41	228.4	12.5	1021	4	US-09-902-540-16773	Sequence 16773, A
42	228	12.5	1089	4	US-09-949-016-9707	Sequence 9707, Ap
43	227.4	12.5	802	4	US-09-823-240A-2	Sequence 2, Appli
44	226.9	12.4	1187	1	US-08-320-559-28	Sequence 28, Appl
45	226.9	12.4	1187	3	US-08-545-860D-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-08-700-607-1
; Sequence 1, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCES/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Consensus
; LIBRARY:
US-08-700-607-1

Query Match 49.6%; Score 904; DB 2; Length 199;
Best Local Similarity 97.3%; Pred. No. 1.6e-33;
Matches 183; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 173 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 232

Db 12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 71
QY 233 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDLVDLSLKPAVL 292
Db 72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDLVDLSLKPAVL 131
QY 293 MVVFTYVGFALFNGLLTLLIALSLFSIPVIYERHQQVQIDHYLGLANKSVKDMAKIOAKI 352
Db 132 MVVFTYVGFALFNGLLTLLIALSLFSIPVIYERHQQVQIDHYLGLANKSVKDMAKIOAKI 191
QY 353 PGLKRRAD 360
Db 192 PGLKRRAE 199

RESULT 2
US-09-949-016-9124
; Sequence 9124, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9124
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9124

Query Match 49.6%; Score 904; DB 4; Length 201;
Best Local Similarity 97.3%; Pred. No. 1.6e-33;
Matches 183; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 173 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 232
Db 14 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 73
QY 233 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDLVDLSLKPAVL 292
Db 74 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDLVDLSLKPAVL 133
QY 293 MVVFTYVGFALFNGLLTLLIALSLFSIPVIYERHQQVQIDHYLGLANKSVKDMAKIOAKI 352
Db 134 MVVFTYVGFALFNGLLTLLIALSLFSIPVIYERHQQVQIDHYLGLANKSVKDMAKIOAKI 193
QY 353 PGLKRRAD 360
Db 194 PGLKRRAE 201

RESULT 3
US-08-700-607-5
; Sequence 5, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 776 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307307
US-08-700-607-5
Query Match 45.3%; Score 826.3; DB 2; Length 776;
Best Local Similarity 27.7%; Pred. No. 7e-29;
Matches 195; Conservative 52; Mismatches 91; Indels 367; Gaps 17;
QY 10 VSSSTDS-----PPR-----19
Db 85 VSSAMDHFTSTSKDGEVCYTSLSIDICYPPQEDSTYFTGLOKENGHVITISESPEELG 144
QY 20 -PPP-----AFKQFVTEPED 34
Db 145 TPGSLPDVPGIESKGLFSSDGIEMTPAESTEVNKKILADPLDQWKAETKIDITRPEE 204
QY 35 EDEEEDEDEED-----DED-----50
Db 205 VKHQHQHPELEDKDLDFKNKQTDISIKPEGVREPKAPVKGKIHKHLLLESTFAPVI 264
QY 51 -----LEEL-55
Db 265 DDLSEORRAPQITTPVKITLITEIPSVETTTQKTPKQDICLKPSPTVPTVTVSEPE 324
QY 56 -----VLERKPAAGLS-----66
Db 325 DDPSPGSIPTSPSGTSPSAESQCKGISSEDELIITAKEAKGLSYETAENPRPVQGLADRP 384
QY 67 ---AAAVPPAAAPLLDFSSDSV-----PPA 89
Db 385 EVKARSGPPTIPSP-LDHEASSAEGSDSEIELVSDPMAAEDALPSGVVFGHVGPPPS 443
QY 90 PRGPL-----PAAPPA-----100
Db 444 PASPSIQYSILREEREAEALDSELIIESCDASSASESPKREQDSPMKPSALDAIREETG 503
QY 101 --APERQPS-----WERSPAAAPAPSLPPA-----AAVLSKLPEDD-----E 135
Db 504 VRAEERAFSRRLAEPGSLFDYPSTEPQPGFELPGDGALEPETPMLPK-PEEESSSNQ 562
QY 136 PPAREPPPPPPAGASPLABPAAPPSTPAAPKRGSGSSVVLLYWRDIKKTGVVFGASLFL 195
Db 563 SPATKGPGLG-----PGAPPPPLFLNKKQ-----AIDLLYWRDIKKTGVVFGSFLLL 611

```

504 VRAERAPSRGLAEPQSLFDYPSTEPQGPDELPPGDALEPETPMLPRK-PEEDSSNQ 562
136 PPAPPPPPAGASPLAEPAPSTPAAPKRRGSGSVVDLLYYWRDIKKTGVFGASLFL 195
563 SPAATKGGPLG-----PGAPPLLEFLNKQK-----AIDLLYYWRDIKQTGIVFGSFLLL 611
196 LLSLTSVSIYSTAYIALALISLTVISPRIYKGVTOAQKSDGHPHFRAYLESEVAISEEL 255
612 LFSLTSQTSVSVVAYLALALSATISPRIYKSVLQAVQKTDGHPHFKAYLEILTSLSEQ 671
256 VQKYSNALGHVNSTIKELRRLFLVDDLVDSLKEAVLMWVYVYGALFNGLTLLTILALIS 315
672 IQKYTDCLQFVNSTLKLRLFLVQDLVDSLKEAVLMWLLTYVYGFNGLTLLLMVVVS 731
316 LFSIPVIYERHQVQIDHYLGLANKSVKMDMAKIOAKTGPLKRRKAD 360
732 MFTLPVYVYVHQAIQIDQYGLVRTHINAVVAKIOAKIPGAKRHA 776

RESULT 5
US-09-949-016-9180
; Sequence 9180, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 9180
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9180

```

```

Query Match      44.8%; Score 816.7; DB 4; Length 439;
Best Local Similarity 40.6%; Pred. No. 6.4e-29;
Matches 182; Conservative 52; Mismatches 101; Indels 113; Gaps 13;

  2 ED-----IDQSLVSSSTDSPPRP-----PPAFKYQVTPTEDEDEEE 41
    ||      ||      ||      ||      ||      ||      ||      ||
    ||      ||      ||      ||      ||      ||      ||      ||
  16 EDLITAIKEAGLSYTAENPRPVGQLADRPEVKARSGPPT-----IPSLDHEASSAE 70
    ||      ||      ||      ||      ||      ||      ||      ||
    ||      ||      ||      ||      ||      ||      ||      ||
  42 EDEEDEDLELEVLERKPAAGLSA-----AAVPPAAAPLPLDFS----- 82
    ||      ||      ||      ||      ||      ||      ||      ||
    ||      ||      ||      ||      ||      ||      ||      ||
  71 SGDSE-----ELVSEDPMABADALPSGVFGVHGPPSPASPASIQYSILREBERA 123
    ||      ||      ||      ||      ||      ||      ||      ||
    ||      ||      ||      ||      ||      ||      ||      ||
  83 -----SDSVPPAPRGPLPAAPPA-----APEROPS----- 107
    ||      ||      ||      ||      ||      ||      ||      ||
    ||      ||      ||      ||      ||      ||      ||      ||
  124 ELDSGLIIESCDASSASEESPKREQDSPMKPSALDAIRETGVRABEERAPSRGIAEPG 183
    ||      ||      ||      ||      ||      ||      ||      ||
    ||      ||      ||      ||      ||      ||      ||      ||
  108 ---WERSPAAPASLPPA-----AAVLSPKLPEDD---EPPARPPPPPPAGASPLA 152
    ||      ||      ||      ||      ||      ||      ||      ||
    ||      ||      ||      ||      ||      ||      ||      ||
  184 SFLDYFSTPEQFGPELPPGGALEBPETMLPRK-PEEDSSNSQPAATKGPGPLG----- 237
    ||      ||      ||      ||      ||      ||      ||      ||
    ||      ||      ||      ||      ||      ||      ||      ||
  153 EPAAAPPSTPAAPKRRGGSSVVDLLYWRDLKKTGWFGASLFLLLSLTFVSIVSVTAYIA 212
    ||      ||      ||      ||      ||      ||      ||      ||
    ||      ||      ||      ||      ||      ||      ||      ||
  238 -PGAPPLLLFNKQK-----AIDLULYWRDLKQTGIVFGSFLLLLSLTFQSVSVVWVAYLA 291
    ||      ||      ||      ||      ||      ||      ||      ||
    ||      ||      ||      ||      ||      ||      ||      ||
  213 LALLSVTISFRIYKGVIAIQKSDGEHPFRAYLESEVAISEELVQKYSNALGHVNSTIK 272
    ||      ||      ||      ||      ||      ||      ||      ||
    ||      ||      ||      ||      ||      ||      ||      ||
  292 LAALSATISFRIYKSVIAQVKTDGEHPFKAYLELEITLSQEQIKYKTDCLQFYVNSTLK 351
    ||      ||      ||      ||      ||      ||      ||      ||
    ||      ||      ||      ||      ||      ||      ||      ||
  273 ELRLFLVDLVDLSIKFAVLMMWVTVYVGALENGLITLLILALISLFGIPVIYERHQVQIDH 332
    ||      ||      ||      ||      ||      ||      ||      ||
    ||      ||      ||      ||      ||      ||      ||      ||

```

Db 352 E1URRFLV00LVDSLKFVALLMULLTYVGALENGLTLLMAVSMETLPVVYKHAQIQD 411

Qy 333 YLGLANKSVKDAMAKIQAKIPGLKPKAD 360
 |||| : ||||| : ||||| : ||||| :
 Db 412 YLGLVRTHINAVVAKIQAKIPGAKRHA 439

RESULT 6
US-08-700-607-6
; Sequence 6, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304

Query Match 43.3%; Score 790; DB 2; Length 356;
Best Local Similarity 44.1%; Pred. No. 7e-28;
Matches 177; Conservative 47; Mismatches 87; Indels 90; Gaps 15;

Qy		2	EIDQSLVS-SSTOSP	RPP--PAFKYQVTFPEDEE-DEE-----EEDEE	15	
Db		4	EDALPSGYVFGHVGPPSPASPGIOYSILIREARELDSLIIESCDASSASEPRK	63	:	
Qy		46	EDDEDLEELVLERPAAGLSAAAVPAAAAAPLLDFSSDSV-	-PPAARGPL	94	
Db		64	EQS-----PPMKPSAL-	DAREETGVABERAPSRRG--	95	
Qy		95	PAAPPAA---PERQFSWERSAAPAPSLPPA---	AALFVKSLPEDD----	BPPAR	139
Db		96	-LAEPGSGLDYSTEPQ-----	PGPELPFGDGALREPETMUPRK-PEEDSSSNQPAA	146	
Qy		140	PPPPPAGASPLAEPAASPPTAAPAKRGGSSVVULLYYWRDIKTQTVFGASLFLLSL	199		
Db		147	TKGPGPLG----FCADPPPLLKNOK-----	AIDLYYWRDIKTQTVFGSFLLLFSL	195	

200	TVFVSIVSVTAIALALISVTSIPRIYKGVIOAQKSDGHPFRAYLESEVAISEELVQKY	259
Qy	: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :	
Db	196 TQFSVSVVAVLAAALSATSIPRIYKSVLQAVQKTDEGHPFKAYLELEITLSQEIQIKY	255
260	SNSALGHVNSTIKELRRLFLVDLDLSKFANVMWFTYYVGALFNGLTLLILALISLPSI	319
Qy	:: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :	
Db	256 TDCLQFYVNSTLKELRRLFLVDLDLSKFANVMWLLTYVGALFNGLTLLMAVSMFTL	315
320	PVIYERHQVQIDHYHGLANKSVKDAMAKIOAKIPGLKRKAD	360
Qy	:: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :	
Db	316 PVVYVKHQAOIQDYLGLVRTHINAVAKIOAKIPGARHAE	356

```

RESULT 7
US-08-700-607-7
; Sequence 7, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307311
;
US-08-700-607-7

```

Query Match 37.5%; Score 683; DB 2; Length 208;
Best Local Similarity 67.4%; Pred. No. 1.8e-23;
Matches 128; Conservative 31; Mismatches 31; Indels 0; Gaps 0;

[illegible]

[illegible]

```

; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

```

```

Query Match      29.6%; Score 539.9; DB 4; Length 168;
Best Local Similarity 59.3%; Pred. No. 3.6e-17;
Matches 99; Conservative 36; Mismatches 31; Indels 1; Gaps 1;

QY 195 LLLSLTVFSIVSTAYIALALLSVTISPRIYKGVIOAIQKSDGHPFRAYLSEVAISEE 254
Db 1 MLLSLAFAFVSIVSVYLLIALLSVTISPRIYKSVIOAQVQKSEGHFKAYLDVDITLSE 60

QY 255 LVQKYSNSALGHVNSTIKELRLFLVDDLVLSKFAVLMWVTYVYVGALENGHTLLILALI 314
Db 61 AFHYNMAAMVHNRALKLIIEFLVEDLVLSKLAFLMWTYVYVGALENGHTLLILABEL 120

QY 315 SLFSPVIVYERHQQVQIDHYGLANKSVKDMAKIQAKIPGL-KRXAD 360
Db 121 LIFSVPVIVYKTKYQIDHYVGIARDQTKSIVEIKIQAKIPGIAXKAE 167

```

```

RESULT 13
US-09-270-767-45132
; Sequence 45132, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 45132
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45132

```

```

Query Match      28.6%; Score 522; DB 4; Length 219;
Best Local Similarity 50.5%; Pred. No. 3.8e-16;
Matches 95; Conservative 43; Mismatches 50; Indels 0; Gaps 0;

QY 166 RRGSGSVVDLYWRDVKTKGVVFGASLFLLSLVTVFSIVSVYATIALALLSVTISFRIY 225
Db 16 RQMSNRLLSLIYWRDVKKSGIVFGAGLITLAAISSFSVISFVAVLSLTFLFTGVAFRY 75

QY 226 KGVIQAIQKSDGHPFRAYLSEVAISELVOKYSNSALGHVNSTIKELRLFLVDDLYD 285
Db 76 KSVTQAVQKNEGHPKFDLDTLSHKBKQVNIAGVAHNGFISELRRLFLVEDIID 135

QY 286 SLKFAVLMWVTYVYVGALENGHTLLILALISLFSIPVYERHQQVQIDHYGLANKSVKDM 345
Db 136 SIKFGVILWVTYVYVGALENGHTLLILALISLFSIPVYERHQQVQIDHYGLANKSVKDM 345

```

```

QY 346 AKIQAKIP 353
Db 196 DKIRVAIP 203

RESULT 14
US-09-513-999C-6304
; Sequence 6304, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6304
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-6304

Query Match      15.7%; Score 286.8; DB 4; Length 68;
Best Local Similarity 85.7%; Pred. No. 1.9e-06;
Matches 60; Conservative 4; Mismatches 4; Indels 2; Gaps 2;

QY 1 MEDIDQSLVSGSTDSPPRPFPAPFYQVTPEDDEDEDEDEDEDEDEDEDEDEDEDELEVLK 60
Db 1 MEDLDQSLVSGSS-DSPRPQAPFYQVTPEDDEDEDEDEDEDEDEDEDEDEDELEVLK 58

QY 61 PAAGLSAAAV 70
Db 59 PAAGLSAAAPV 68

```

```

RESULT 15
US-09-149-476-411
; Sequence 411, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597

```

[illegible]

; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 15.7%; Score 286; DB 4; Length 92;
Best Local Similarity 56.0%; Pred. No. 3.6e-06;
Matches 51; Conservative 21; Mismatches 19; Indels 0; Gaps 0;
Qy 261 NSALGHVNSTIKELRLEFLVDLVDLSLKEAVLMMVETVYVGALENGTLTLLALISLFSIP 320
Db 2 NAAMVHINRALKLITIKLEFLVEDLVDLSKLAVFNMWLTYYGAVFNGITLLILAEELLFSVP 61
Qy 321 VIYERHQVQIDHYHGLANKSVKDAMAKIOAK 351
Db 62 IVEKYKQIDHYVGIARDQTKSIVEKIPSK 92

Search completed: June 23, 2005, 10:17:47
Job time : 32.4577 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2005, 09:56:59 ; Search time 108.849 Seconds
(without alignments)
1271.831 Million cell updates/sec

Title: US-09-830-972-2-FUSED

Perfect score: 1823

Sequence: 1 MEDIDQSSLVSSSTDSPPRP.....VKDAMAKIOAKIPGLRRKAD 360

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.1

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1817	99.7	360	9 US-09-893-348-20	Sequence 20, Appl
2	1817	99.7	360	16 US-10-810-653-20	Sequence 20, Appl
3	1808.1	99.2	379	14 US-10-205-194-164	Sequence 164, App
4	1732.7	95.0	1163	9 US-09-893-348-18	Sequence 18, Appl
5	1732.7	95.0	1163	16 US-10-810-653-18	Sequence 18, Appl
6	1637	89.8	1162	16 US-10-633-423-10	Sequence 10, Appl
7	1637	89.8	1162	16 US-10-427-741-10	Sequence 10, Appl
8	1622.9	89.0	1163	15 US-10-267-502-431	Sequence 431, App
9	1603.3	87.9	373	9 US-09-789-386-6	Sequence 6, Appl
10	1603.3	87.9	373	9 US-09-765-203-6	Sequence 6, Appl
11	1603.3	87.9	373	9 US-09-893-348-24	Sequence 24, Appl

12	1603.3	87.9	373	14 US-10-060-036-72	Sequence 72, Appl
13	1603.3	87.9	373	15 US-10-408-967-8	Sequence 8, Appl
14	1603.3	87.9	373	16 US-10-810-653-24	Sequence 24, Appl
15	1603.3	87.9	373	17 US-10-347-663-6	Sequence 6, Appl
16	1595.3	87.5	373	16 US-10-466-258-4	Sequence 4, Appl
17	1518.4	83.3	1192	9 US-09-789-386-2	Sequence 2, Appl
18	1518.4	83.3	1192	9 US-09-758-140-6	Sequence 6, Appl
19	1518.4	83.3	1192	9 US-09-893-348-23	Sequence 23, Appl
20	1518.4	83.3	1192	9 US-09-972-599A-6	Sequence 6, Appl
21	1518.4	83.3	1192	14 US-10-060-036-71	Sequence 71, Appl
22	1518.4	83.3	1192	15 US-10-267-502-429	Sequence 429, App
23	1518.4	83.3	1192	16 US-10-327-213-9	Sequence 9, Appl
24	1518.4	83.3	1192	16 US-10-466-258-9	Sequence 9, Appl
25	1518.4	83.3	1192	16 US-10-810-653-23	Sequence 23, Appl
26	1511.4	82.9	1192	15 US-10-408-967-7	Sequence 7, Appl
27	921	50.5	199	9 US-09-893-348-21	Sequence 21, Appl
28	921	50.5	199	16 US-10-810-653-21	Sequence 21, Appl
29	904	49.6	199	9 US-09-893-348-25	Sequence 25, Appl
30	904	49.6	199	15 US-10-660-946-1	Sequence 1, Appl
31	904	49.6	199	16 US-10-810-653-25	Sequence 25, Appl
32	897	49.2	199	15 US-10-408-967-9	Sequence 9, Appl
33	895	49.1	199	11 US-09-978-360A-467	Sequence 467, App
34	864	47.4	199	16 US-10-466-258-11	Sequence 11, Appl
35	826.3	45.3	776	15 US-10-660-946-5	Sequence 5, Appl
36	826.3	45.3	776	15 US-10-267-502-430	Sequence 430, App
37	826.3	45.3	776	16 US-10-723-860-1481	Sequence 1481, App
38	823.2	45.2	780	15 US-10-267-502-432	Sequence 432, App
39	807.4	44.3	777	14 US-10-205-219-93	Sequence 93, Appl
40	790	43.3	356	15 US-10-660-946-6	Sequence 6, Appl
41	687.7	37.7	593	15 US-10-108-260A-2892	Sequence 2892, App
42	683	37.5	208	15 US-10-660-946-7	Sequence 7, Appl
43	679	37.2	266	15 US-10-276-774-2330	Sequence 2330, App
44	672.9	36.9	269	14 US-10-106-698-6222	Sequence 6222, App
45	669	36.7	267	14 US-10-205-194-127	Sequence 127, App

ALIGNMENTS

RESULT 1
US-09-893-348-20
; Sequence 20, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR US
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-20

Query Match 99.7%; Score 1817; DB 9; Length 360;
Best Local Similarity 99.7%; Pred. No. 8.9e-55;
Matches 359; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

477	Db	BERKAQIIITEKTSPTKSNPFLVAIHDSEADYVTTDNLSKVTEAVVATWPEGLTPDLVQEA	536
172	Qy	-----	171
537	Db	CESELNEATGTKIAIYETKVDLVQTSALQBSIYPTAQLCPSEEEAATPSPVLPIVMEA	596
172	Qy	-----	171
597	Db	PLNSLLPSTGASVAQPSASPLEVPSVSYDGIKLEPENPPPYEEAMSVALKTSDSKEIK	656
172	Qy	-----	171
657	Db	EPESEFNAAQEAEBAPYISIACDLIKETKLTSTEPSPEFSNYSEIAKFEKSPVDCHELVDSD	716
172	Qy	-----	171
717	Db	SPSEPEVDLFSDDSIPEVPQOTQEEAVMLKESLTVSETVTOHKHKBRLSASPOEVGKPY	776
172	Qy	-----	171
777	Db	LESFQPNLHITKDAASNEIPTLTYYKETISLOMBEFTAIYNNDDLLSSKEDKMKSEFTFS	836
172	Qy	-----	171
837	Db	DSSPIEIIIDFPPTFVSAKDDSPKEYTDLEVSNKSEIANVQSGANSLPCSELPCDLSPKNT	896
172	Qy	-----	171
897	Db	YPKDEAHVDEFFSKRSRVSXKVPULLPNVSALESQIEMGNIVPKVLTKBAEKLPSDTE	956
172	Qy	-----SVVDLLYWRDIKKTGVVFGASFLFLLLSLTVFSIVSVTAYIALA	214
957	Db	KEDRSLTAVLSAELNKTSSVVDLLYWRDIKKTGVVFGASFLFLLLSLTVFSIVSVTAYIALA	1016
215	Qy	LLSVTISFRIYKGVIOAIQKSDGHPPRAYLESEVAISEELVKQYSNSALGHVNSTIKEL	274
1017	Db	LLSVTISFRIYKGVIOAIQKSDGHPPRAYLESEVAISEELVKQYSNSALGHVNSTIKEL	1076
275	Qy	RRLFLVDDLDVLSLKFVLMVFTVVGALFNGLTLLIILALISLPSIPVYERHVOQIDHYL	334
1077	Db	RRLFLVDDLDVLSLKFVLMVFTVVGALFNGLTLLIILALISLPSIPVYERHVOQIDHYL	1136
335	Qy	GLANKSVKIDAMAKIOAKIPGLKPKAD	360
1137	Db	GLANKSVKIDAMAKIOAKIPGLKPKAE	1162

RESULT 7

```

RESUL1 /
US-10-427-741-10
; Sequence 10, Application US/10427741
; Publication No. US20040191291A1
; GENERAL INFORMATION:
; APPLICANT: Tohyama, Masaya
; APPLICANT: Yamashita, Toshihide
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION
; FILE REFERENCE: 59150-8023
; CURRENT APPLICATION NUMBER: US/10/427,741
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: JP 2003-92923
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-427-741-10

Query Match      89.8%; Score 1637; DB 16; Length 1162;
Best Local Similarity 29.8%; Pred. No. 1.1e-47;
Matches 348; Conservative 2; Mismatches 6; Indels 810; Gaps 4;

QY 1 MEDIDQSSLVSSSTDSPRPFPFAKTFVTEPDEDEDEDEDEDEDEDELEVLERK 60

```


This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2005, 10:16:50 ; Search time 113.842 Seconds
(without alignments)
1223.045 Million cell updates/sec

Title: US-09-830-972-2-FUSED

Perfect score: 1823

Sequence: 1 MEDIDQSLVSSSTDSPPRP.....VKDAWKIQAKIPGLKRRAD 360

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.1

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1817	99.7	359	AAy71558	AAy71558 Rat Nogo
2	1817	99.7	360	AAy71383	AAy71383 Rat neuro
3	1817	99.7	360	AB881076	AB881076 Rat neuro
4	1812.9	99.4	361	AAy71385	AAy71385 Alternati
5	1808.1	99.2	379	AD885283	AD885283 Rat fooc
6	1732.7	95.0	1163	AAy71310	AAy71310 Rat neuro
7	1732.7	95.0	1163	AAy71384	AAy71384 Alternati
8	1732.7	95.0	1163	AB881074	AB881074 Rat neuro
9	1732.7	95.0	1163	AD026399	AD026399 Rat trunc
10	1732.7	95.0	1163	ADP45572	ADP45572 Rat NogoA
11	1726.7	94.7	1162	AAy71557	AAy71557 Rat Nogo
12	1637	89.8	1162	AD789537	AD789537 Mus muscu
13	1622.9	89.0	1163	AD008105	AD008105 Mouse pol
14	1603.3	87.9	373	AAy53624	AAy53624 A bone ma
15	1603.3	87.9	373	AAy56969	AAy56969 Human MAG
16	1603.3	87.9	373	AAy56969	AAy56969 Human MAG
17	1603.3	87.9	373	AAy56969	AAy56969 Human MAG
18	1603.3	87.9	373	AAy56969	AAy56969 Human MAG
19	1603.3	87.9	373	AAy56969	AAy56969 Human MAG
20	1603.3	87.9	373	AAy56969	AAy56969 Human MAG
21	1603.3	87.9	373	AAy56969	AAy56969 Human MAG
22	1603.3	87.9	373	AAy56969	AAy56969 Human MAG
23	1603.3	87.9	373	AAy56969	AAy56969 Human MAG
24	1595.3	87.5	373	AAy56969	AAy56969 Human MAG
25	1518.4	83.3	1192	AAy56969	AAy56969 Human MAG

26	1518.4	83.3	1192	4	AB882349	AB882349 Human NOG
27	1518.4	83.3	1192	4	AAU04591	AAU04591 Human NOG
28	1518.4	83.3	1192	5	ABG30938	ABG30938 Human NOG
29	1518.4	83.3	1192	5	ABP68600	ABP68600 Human pan
30	1518.4	83.3	1192	5	AB881078	AB881078 Human neu
31	1518.4	83.3	1192	6	ABR59667	ABR59667 Human NOG
32	1518.4	83.3	1192	8	AD008103	AD008103 Human NOG
33	1518.4	83.3	1192	8	ADP45551	ADP45551 Human NOG
34	1518.4	83.3	1192	8	ADP67234	ADP67234 Human NOG
35	1518.4	83.3	1192	8	ADP67234	ADP67234 Human NOG
36	1511.4	82.9	1192	7	ADK67502	ADK67502 Human RTN
37	1511.4	82.9	1192	8	AD026400	AD026400 Human tru
38	1510.8	82.9	1178	3	AAy71311	AAy71311 Human neu
39	1263	69.3	360	4	AAE03987	AAE03987 Human gen
40	1237.7	67.9	1246	4	AAU03328	AAU03328 Novel hum
41	1204.7	66.1	291	4	AAm93484	AAm93484 Human pro
42	1204.7	66.1	291	8	ADL31138	ADL31138 Human pro
43	1013.8	55.6	973	8	ADQ16420	ADQ16420 Fusion pr
44	1012.1	55.5	983	6	ABU11573	ABU11573 Human MDD
45	1010.8	55.4	893	3	AAy95012	AAy95012 Human sec

ALIGNMENTS

RESULT 1

AAy71558
ID AAy71558 standard; protein; 359 AA.

XX AAy71558;

DT 02-NOV-2000 (first entry)

DE Rat Nogo A protein fragment used in the construction of mutant Nogo-B.

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening; mutant; mutein.

OS Rattus sp.

FH Key Location/Qualifiers
Region 1..171

FT /note= "Corresponds to residues 1-171 of rat Nogo A
protein shown in AAY71310"

FT /note= "Corresponds to residues 975-1162 of rat Nogo A
protein shown in AAY71310"

PN WO200031235-A2.

PD 02-JUN-2000.

PF 05-NOV-1999; 99WO-US026160.

PR 06-NOV-1998; 98US-0107446P.

XX (SCHW/) SCHWAB M E.

XX (CHEN/) CHEN M S.

PI Schwab ME, Chen MS;

XX WPI; 2000-400052/34.

XX Nogo proteins and nucleic acids useful for treating neoplastic disorders
of the central nervous system and inducing regeneration of neurons.

PS Example; Page; 122pp; English.

XX

QY 301 ALFNGTLTLLILALISLFSIPVIYERHQQVQIDHYLGLANKSVKDMAKIQAKIPGLKRRAD 360
DB 301 ALFNGTLTLLILALISLFSIPVIYERHQQVQIDHYLGLANKSVKDMAKIQAKIPGLKRRAD 360

RESULT 4
AAAY71385
ID AAAY71385 standard; protein; 361 AA.
AC AAAY71385;
DT 02-NOV-2000 (first entry)
XX Alternative version of rat neurite growth inhibitor Nogo B.
XX Rat; neurite growth inhibitor; Nogo B; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; benign dysproliferative disorder; treatment;
KW structural plasticity; screening.
XX Rattus sp.
XX Key Location/Qualifiers
XX Region 1..172
FT /note= "Corresponds to amino acids 1-172 of Nogo A
FT protein shown in AAAY71310"
FT Inhibitory-site 1..171
FT /note= "Inhibits NIH 3T3 fibroblast spreading"
FT Modified-site 30
FT /note= "Casein kinase II site"
FT Region 31..58
FT /note= "Acidic region"
FT Region 173..361
FT /note= "Corresponds to amino acids 975-1163 of Nogo A
FT protein (AAAY71310)"
FT Region 174..361
FT /note= "This region is common to Nogo A, B and C
FT isoforms"
FT Domain 186..221
FT /label= Transmembrane domain
FT /note= "C-terminal hydrophobic region"
FT Modified-site 222
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 269..271
FT /note= "Asn is N-glycosylated"
FT Modified-site 271
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 287
FT /note= "Protein kinase C (PKC) site"
FT Domain 288..323
FT /label= Transmembrane domain
FT /note= "C-terminal hydrophobic region"
FT Modified-site 339..341
FT /note= "Asn is N-glycosylated"
FT Modified-site 341
FT /note= "Protein kinase C (PKC) site"
XX WO200031235-A2.
PN
XX
PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US026160.
XX
PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;

XX WPI; 2000-400052/34.
XX
XX Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX
XX Claim 4; Page; 122pp; English.
XX
CC The present sequence is an alternative version of rat Nogo B protein
CC which is a potent neural cell growth inhibitor and is free of all central
CC nervous system (CNS) myelin material with which it is native
CC associated. The Nogo B transcript arises as a result of alternative
CC splicing of Nogo gene. Nogo proteins and fragments displaying neurite
CC growth inhibitory activity are used in the treatment of neoplastic
CC disease of the CNS e.g. glioma, glioblastoma, medulloblastoma,
CC craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic
CC neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma
CC and degenerative nerve diseases e.g. Alzheimer's and Parkinson's
CC diseases. Therapeutics which promote Nogo activity can be used to treat
CC or prevent hyperproliferative or benign dysproliferative disorders e.g.
CC psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic
CC acids can be used to inhibit production of Nogo protein to induce
CC regeneration of neurons or to promote structural plasticity of the CNS in
CC disorders where neurite growth, regeneration or maintenance are deficient
CC or desired. The animal models can be used in diagnostic and screening
CC methods for predisposition to disorders and to screen for or test
CC molecules which can treat or prevent disorders or diseases of the CNS.
CC Note: The present sequence is not given in the specification but is
CC derived from Nogo A protein sequence (AAAY71310) and corresponds to
CC residues 1-172 fused to 975-1163 of Nogo A. This sequence is an
CC alternative version of the Nogo B sequence (see AAAY71383) described in
CC the specification as being residues 1-172 fused to C-terminal 188 amino
CC acids (residues 976-1163) of Nogo A. SEQ ID numbers 35-42 are referred in
CC claim 32 and SEQ ID NO: 29 in disclosure of the specification. However
CC the specification does not include sequences for these SEQ ID numbers
XX
XX SQ Sequence 361 AA;
Query Match 99.4%; Score 1812.9; DB 3; Length 361;
Best Local Similarity 99.7%; Pred. No. 4.4e-65;
Matches 360; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MEDIDQSSLSVSSSTDSPPRPPPAFKYQVTPPEDEDEDEDEDEDEDEDEDEDEDELEVLK 60
DB 1 MEDIDQSSLSVSSSTDSPPRPPPAFKYQVTPPEDEDEDEDEDEDEDEDEDEDEDELEVLK 60
QY 61 PAAGLSAAAVPAAAPLLDFSSDSVPPAPRGPLPAAAPAPAPAPAPAPAPAPAPAPAPSLP 120
DB 61 PAAGLSAAAVPAAAPLLDFSSDSVPPAPRGPLPAAAPAPAPAPAPAPAPAPAPAPAPSLP 120
QY 121 PAAAVLPKLPEDDEPPAPPPPPPPAGASPLAEPAPAPSTPAAPKRRGSGS-SVVDLLYW 179
DB 121 PAAAVLPKLPEDDEPPAPPPPPPPAGASPLAEPAPAPSTPAAPKRRGSGSVVDLLYW 180
QY 180 RDIKKTGVVFGASLFLLLSLTFSVSVTAYIALALLSVTISFRYKGVQIAQKSDGH 239
DB 181 RDIKKTGVVFGASLFLLLSLTFSVSVTAYIALALLSVTISFRYKGVQIAQKSDGH 240
QY 240 PFRAYLESEVAISELQKYSNLSALGHVNSTIKELRRLFLVDDLDVSLKFAVLWVFTV 299
DB 241 PFRAYLESEVAISELQKYSNLSALGHVNSTIKELRRLFLVDDLDVSLKFAVLWVFTV 300
QY 300 GAFNGLTLLILALISLFSIPVIYERHQQVQIDHYLGLANKSVKDMAKIQAKIPGLKRR 359
DB 301 GAFNGLTLLILALISLFSIPVIYERHQQVQIDHYLGLANKSVKDMAKIQAKIPGLKRR 360
QY 360 D 360
DB 361 D 361
RESULT 5
ADB85283

FT /note= "Protein kinase C (PKC) site"
 FT 694. .696
 FT /note= "Asn is N-glycosylated"
 FT 715
 FT /note= "Casein kinase II site"
 FT 762. .1163
 FT /note= "used as immunogen to generate antibody AS Bruna"
 FT 784
 FT /note= "Protein kinase C (PKC) site"
 FT 821
 FT /note= "Protein kinase C (PKC) site"
 FT 850
 FT /note= "Protein kinase C (PKC) site"
 FT 855
 FT /note= "Protein kinase C (PKC) site"
 FT 863
 FT /note= "Casein kinase II site"
 FT 868
 FT /note= "Protein kinase C (PKC) site"
 FT 893
 FT /note= "Protein kinase C (PKC) site"
 FT 912. .914
 FT /note= "Asn is N-glycosylated"
 FT 925. .927
 FT /note= "Asn is N-glycosylated"
 FT 954
 FT /note= "PKC and casein kinase II sites"
 FT 956
 FT /note= "PKC and casein kinase II sites"
 FT 975. .1162
 FT /note= "This region is not essential for inhibitory activity"
 FT 976. .1163
 FT /note= "C-terminal common region found in Nogo A, B and C isoforms"
 FT 988. .1023
 FT /label= Transmembrane domain
 FT /note= "C-terminal hydrophobic region specifically described in claim 16"
 FT 1024
 FT /note= "Protein kinase C (PKC) site"
 FT 1071. .1073
 FT /note= "Asn is N-glycosylated"
 FT 1073
 FT /note= "Protein kinase C (PKC) site"
 FT 1089
 FT /note= "Protein kinase C (PKC) site"
 FT 1090. .1125
 FT /label= Transmembrane domain
 FT /note= "C-terminal hydrophobic region specifically described in claim 16"
 FT 1141. .1143
 FT /note= "Asn is N-glycosylated"
 FT 1143
 FT /note= "Protein kinase C (PKC) site"
 FT WO200031235-A2.
 FT 02-JUN-2000.
 FT 05-NOV-1999; 99WO-US026160.
 FT 06-NOV-1998; 98US-0107446P.
 FT (SCHW/) SCHWAB M E.
 FT (CHEN/) CHEN M S.
 FT Schwab ME, Chen MS;
 FT WPI: 2000-400052/34.
 FT N-PSDB; AAD01173.
 FT Nogo proteins and nucleic acids useful for treating neoplastic disorders

PT of the central nervous system and inducing regeneration of neurons.
 XX Claim 3; Fig 2A; 122pp; English.
 CC The present sequence is a rat Nogo A protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) myelin material with which it is naturally associated. The protein was derived from a cDNA generated by fusing RO18U37-3, R1-3U21 cDNAs isolated from hexanucleotides-primed rat brain stem/spinal cord library, and O118 cDNA from an oligo d(T)-primed rat oligodendrocyte library. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. Note: The present sequence designated as SEQ ID NO: 2 is stated to be the same as the sequence shown in Fig. 13 (see AAY71384) of the specification. However, this sequence does not match the sequence given in Fig. 13. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However, the specification does not include sequences for these SEQ ID numbers
 XX Sequence 1163 AA;
 SQ
 Query Match 95.0%; Score 1732.7; DB 3; Length 1163;
 Best Local Similarity 31.0%; Pred. No. 5.7e-61;
 Matches 360; Conservative 0; Mismatches 0; Indels 803; Gaps 1;
 QY 1 MEDIDQSLVSSSTDSPPRPAPKYPQVTPPEDEDEDEDEDEDEDEDEDEDEDELEVLERK 60
 DB 1 MEDIDQSLVSSSTDSPPRPAPKYPQVTPPEDEDEDEDEDEDEDEDEDEDELEVLERK 60
 QY 61 PAAGLSAAAVPAAAPLLDFSSDVPAPRGPPLPAPAPAPAPRQPSWERSPAAAPSLP 120
 DB 61 PAAGLSAAAVPAAAPLLDFSSDVPAPRGPPLPAPAPAPAPRQPSWERSPAAAPSLP 120
 QY 121 PAAVLPKLPEDPEPPAPPPPPAGASPLAEPAPSTTAAAPKRGSGS----- 171
 DB 121 PAAVLPKLPEDPEPPAPPPPPAGASPLAEPAPSTTAAAPKRGSGSVDETLFALP 180
 QY 172 ----- 171
 DB 181 AASEVPISPSSAEKIMDLMEQPGNTVSSQEDPFPVLLLETAASLPSLSTVSKFHEGYL 240
 QY 172 ----- 171
 DB 241 GNLSAVSSSEGTIBETLINEASKELPERATNPFVNRDLAEFSELEYSEMGSFPGKPGKES 300
 QY 172 ----- 171
 DB 301 AILVENTKEVIVRSKDKEDLVCSAALHSPQSPGVKEDRVVSPKKTWDIENEMQMSVVA 360
 QY 172 ----- 171
 DB 361 PVREYADFKPFEQAWKVDYEGSRDVLAAANVESKVDKCIEDSLQKSLGKDSGR 420
 QY 172 ----- 171
 DB 421 NEDASFPSTPEPVKDSRRAYITCASFTSATESTTANTFPFLLEDHTSENKTDKIEERKA 480
 QY 172 ----- 171
 DB 481 QIITEKTSPTKSNPFLVAVQDSEADYVTTDTLSKYTEAAVSNMPEGLTFLDVLQACESEL 540

QY	172	-----	171	FT	Region	172..259	/note="This region is not essential for inhibitory activity"
Db	541	NEATGKIAYETKVDLVQTSIAQESLYPTAQLCPSFEAEATPSPVLPDIWMEAPLNSL	600	FT	Misc-difference	223	
QY	172	-----	171	FT		/label= Unknown	
Db	601	LPSAGASVVQPSVSPLEAPPVSYDSIKLEPENPPPYEAMNVALKALGTKEIKEPSPF	660	FT	Modified-site	233	/note="Protein kinase C (PKC) site"
QY	172	-----	171	FT	Modified-site	242..244	/note="There is Leu at this position in the sequence shown in AAY71310"
Db	661	NAAVQTEAPYISACDLIKETKLTSPSPDFSNYSYSEIAKFEKSVPEHAELVEDSPSE	720	FT	Modified-site	291	/note="Asn is N-glycosylated"
QY	172	-----	171	FT	Modified-site	295	/note="Protein kinase C (PKC) site"
Db	721	PVDLFSDDSIPEVPQTEAEVLMKESLTVSETVAQHKEERLSASPOSLGPKYLESPQ	780	FT	Modified-site	295	/note="Protein kinase C (PKC) site"
QY	172	-----	171	FT	Misc-difference	404	/note="There is Ile at this position in the sequence shown in AAY71310"
Db	781	NLHSTKDAASNDIPTLTKEKISLQMEENTAIYSNDLLSSKEDKIKESETFSDSSPIE	840	FT	Modified-site	436	/note="Protein kinase C (PKC) site"
QY	172	-----	171	FT	Modified-site	468..470	/note="Asn is N-glycosylated"
Db	841	IIDEPTFVSAXDGPKLAKKEYTDLEVSDKSEIANIQSGADSLPCLPLCDLSFKNIYPK	900	FT	Misc-difference	469	/label= Unknown
QY	172	-----	171	FT		/note="There is Lys at this position in the sequence shown in AAY71310"	
Db	901	DEVHVSDEFSENRSVSKASISPSNVSALEPQTEMGSIYKSKSLTKAEAKKLPSDTEKED	960	FT	Modified-site	484	/note="Protein kinase C (PKC) site"
QY	172	-----	217	FT	Modified-site	488	/note="Protein kinase C (PKC) site"
Db	961	RLSVAVLSNELSKTSVVDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTVAYIALALLS	1020	FT	Modified-site	502	/note="Protein kinase C (PKC) site"
QY	218	VTISPRIYKGVIOAIQKSDGHPFRAYLSEVAISEELVQKYSNLSALGHVNSTIKELRRL	277	FT	Inhibitory-site	542..722	/note="Casein kinase II site"
Db	1021	VTISPRIYKGVIOAIQKSDGHPFRAYLSEVAISEELVQKYSNLSALGHVNSTIKELRRL	1080	FT	Modified-site	576	/note="Casein kinase II site"
QY	278	FLVDDLVDLSKFAVLMMWFTYTYGALFNGLTILILALISLFSIPVIYERHQQVIDHYLGIA	337	FT	Peptide	623..640	/note="used as immunogen to generate antibody AS 472"
Db	1081	FLVDDLVDLSKFAVLMMWFTYTYGALFNGLTILILALISLFSIPVIYERHQQVIDHYLGIA	1140	FT	Modified-site	626	/note="Protein kinase C (PKC) site"
QY	338	NKSVKDMAKIOAKIPGLKRRAD	360	FT	Misc-difference	661	/note="There is Asn at this position in the sequence shown in AAY71310"
Db	1141	NKSVKDMAKIOAKIPGLKRRAD	1163	FT	Modified-site	694..696	/note="Asn is N-glycosylated"
RESULT 7				FT	Modified-site	715	/note="Casein kinase II site"
AAV71384				FT	Peptide	762..1163	/note="used as immunogen to generate antibody AS Bruna"
ID AAY71384 standard; protein; 1163 AA.				FT	Modified-site	784	/note="Protein kinase C (PKC) site"
AC AAY71384;				FT	Misc-difference	820	/note="There is Leu at this position in the sequence shown in AAY71310"
DT 02-NOV-2000 (first entry)				FT	Modified-site	821	/note="Protein kinase C (PKC) site"
DE Alternative version of rat neurite growth inhibitor Nogo A.				FT	Modified-site	850	/note="Protein kinase C (PKC) site"
XX Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;				FT	Modified-site	855	/note="Protein kinase C (PKC) site"
KW central nervous system; neoplastic disease; antiproliferative; glioma;				FT	Modified-site	863	/note="Protein kinase C (PKC) site"
KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;				FT	Modified-site	868	/note="Casein kinase II site"
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;				FT	Modified-site	893	/note="Protein kinase C (PKC) site"
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;				FT	Modified-site	912..914	/note="Asn is N-glycosylated"
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;				FT	Modified-site	925..927	/note="Asn is N-glycosylated"
XX structural plasticity; screening.				FT	Modified-site	954	/note="PKC and casein kinase II sites"
OS Rattus sp.				FT	Modified-site	956	/note="PKC and casein kinase II sites"
XX				FT			
XX				FT			
Key Location/Qualifiers				FT			
FT Inhibitory-site 1..171				FT			
FT /note="Inhibits NIH 3T3 fibroblast spreading"				FT			
FT Modified-site 30				FT			
FT /note="Casein kinase II site"				FT			
FT Region 31..58				FT			
FT /note="Acidic region"				FT			

Region	975. .1162	976. .1163	977. .1164	978. .1165	979. .1166	980. .1167	981. .1168	982. .1169	983. .1170	984. .1171	985. .1172	986. .1173	987. .1174	988. .1175	989. .1176	990. .1177	991. .1178	992. .1179	993. .1180	994. .1181	995. .1182	996. .1183	997. .1184	998. .1185	999. .1186	1000. .1187	1001. .1188	1002. .1189	1003. .1190	1004. .1191	1005. .1192	1006. .1193	1007. .1194	1008. .1195	1009. .1196	1010. .1197	1011. .1198	1012. .1199	1013. .1200	1014. .1201	1015. .1202	1016. .1203	1017. .1204	1018. .1205	1019. .1206	1020. .1207	1021. .1208	1022. .1209	1023. .1210	1024. .1211	1025. .1212	1026. .1213	1027. .1214	1028. .1215	1029. .1216	1030. .1217	1031. .1218	1032. .1219	1033. .1220	1034. .1221	1035. .1222	1036. .1223	1037. .1224	1038. .1225	1039. .1226	1040. .1227	1041. .1228	1042. .1229	1043. .1230	1044. .1231	1045. .1232	1046. .1233	1047. .1234	1048. .1235	1049. .1236	1050. .1237	1051. .1238	1052. .1239	1053. .1240	1054. .1241	1055. .1242	1056. .1243	1057. .1244	1058. .1245	1059. .1246	1060. .1247	1061. .1248	1062. .1249	1063. .1250	1064. .1251	1065. .1252	1066. .1253	1067. .1254	1068. .1255	1069. .1256	1070. .1257	1071. .1258	1072. .1259	1073. .1260	1074. .1261	1075. .1262	1076. .1263	1077. .1264	1078. .1265	1079. .1266	1080. .1267	1081. .1268	1082. .1269	1083. .1270	1084. .1271	1085. .1272	1086. .1273	1087. .1274	1088. .1275	1089. .1276	1090. .1277	1091. .1278	1092. .1279	1093. .1280	1094. .1281	1095. .1282	1096. .1283	1097. .1284	1098. .1285	1099. .1286	1100. .1287	1101. .1288	1102. .1289	1103. .1290	1104. .1291	1105. .1292	1106. .1293	1107. .1294	1108. .1295	1109. .1296	1110. .1297	1111. .1298	1112. .1299	1113. .1300	1114. .1301	1115. .1302	1116. .1303	1117. .1304	1118. .1305	1119. .1306	1120. .1307	1121. .1308	1122. .1309	1123. .1310	1124. .1311	1125. .1312	1126. .1313	1127. .1314	1128. .1315	1129. .1316	1130. .1317	1131. .1318	1132. .1319	1133. .1320	1134. .1321	1135. .1322	1136. .1323	1137. .1324	1138. .1325	1139. .1326	1140. .1327	1141. .1328	1142. .1329	1143. .1330	1144. .1331	1145. .1332	1146. .1333	1147. .1334	1148. .1335	1149. .1336	1150. .1337	1151. .1338	1152. .1339	1153. .1340	1154. .1341	1155. .1342	1156. .1343	1157. .1344	1158. .1345	1159. .1346	1160. .1347	1161. .1348	1162. .1349	1163. .1350	1164. .1351	1165. .1352	1166. .1353	1167. .1354	1168. .1355	1169. .1356	1170. .1357	1171. .1358	1172. .1359	1173. .1360	1174. .1361	1175. .1362	1176. .1363	1177. .1364	1178. .1365	1179. .1366	1180. .1367	1181. .1368	1182. .1369	1183. .1370	1184. .1371	1185. .1372	1186. .1373	1187. .1374	1188. .1375	1189. .1376	1190. .1377	1191. .1378	1192. .1379	1193. .1380	1194. .1381	1195. .1382	1196. .1383	1197. .1384	1198. .1385	1199. .1386	1200. .1387	1201. .1388	1202. .1389	1203. .1390	1204. .1391	1205. .1392	1206. .1393	1207. .1394	1208. .1395	1209. .1396	1210. .1397	1211. .1398	1212. .1399	1213. .1400	1214. .1401	1215. .1402	1216. .1403	1217. .1404	1218. .1405	1219. .1406	1220. .1407	1221. .1408	1222. .1409	1223. .1410	1224. .1411	1225. .1412	1226. .1413	1227. .1414	1228. .1415	1229. .1416	1230. .1417	1231
--------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	------

RESULT 11
 AAY71557
 ID AAY71557 standard; protein; 1162 AA.
 AC AAY71557;
 XX
 XX
 DT 02-NOV-2000 (first entry)
 XX
 XX Rat Nogo A truncated protein used in the construction of mutant Nogo-A.
 XX
 KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
 KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; benign dysproliferative disorder; treatment;
 KW structural plasticity; screening; mutant; neuron; regeneration;
 XX
 OS Rattus sp.
 XX
 PN WO200031235-A2.
 XX
 XX 02-JUN-2000.
 PD
 XX
 PF 05-NOV-1999; 99WO-US026160.
 XX
 PR 06-NOV-1998; 98US-0107446P.
 XX
 PA (SCHW/) SCHWAB M E.
 PA (CHEN/) CHEN M S.
 XX
 PI Schwab ME, Chen MS;
 XX
 DR WPI; 2000-400052/34.
 XX
 PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
 PT of the central nervous system and inducing regeneration of neurons.
 XX
 PS Example; Page; 122pp; English.
 XX
 CC The patent relates to neurite growth inhibitor Nogo which is free of all
 CC central nervous system (CNS) myelin material with which it is natively
 CC associated. Nogo proteins and fragments displaying neurite growth
 CC inhibitory activity are used in the treatment of neoplastic disease of
 CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
 CC ependymoma, pinealoma, haemangioblastoma, acoustic neuroma,
 CC oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and
 CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
 CC Therapeutics which promote Nogo activity can be used to treat or prevent
 CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
 CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
 CC used to inhibit production of Nogo protein to induce regeneration of
 CC neurons or to promote structural plasticity of the CNS in disorders where
 CC neurite growth, regeneration or maintenance are deficient or desired. The
 CC animal models can be used in diagnostic and screening methods for
 CC predisposition to disorders and to screen for or test molecules which can
 CC treat or prevent disorders or diseases of the CNS. The present sequence
 CC is a truncated form of rat Nogo A protein shown in AAY71310, which is
 CC used in the construction of mutant Nogo-A. Nogo-A is composed of His-
 CC tag/T7-tag/vector/Nogo-A sequence aa 1-1162. Nogo A deletion mutants were
 CC used for mapping the inhibitory sites of Nogo protein. Major inhibitory
 CC region was identified in the Nogo A sequence from amino acids 172-974,
 CC particularly amino acids 542-722. In addition, N-terminal region 1-171
 CC was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The
 CC present sequence is not given in the specification but is derived from
 CC rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred
 CC in claim 32 and SEQ ID NO: 29 in disclosure of the specification.
 CC However, the specification does not include sequences for these SEQ ID
 CC numbers
 XX
 XX Sequence 1162 AA;

Query Match 94.7%; Score 1726.7; DB 3; Length 1162;
 Best Local Similarity 30.9%; Pred. No. 1e-60;
 Matches 359; Conservative 0; Mismatches 0; Indels 803; Gaps 1;
 QY 1 MEDIDQSSLVSSSTDSPPRPAPAFKYQVTPPEDEDEDEDEDEDEDEDEDEDEDELEVLERK 60
 DB 1 MEDIDQSSLVSSSTDSPPRPAPAFKYQVTPPEDEDEDEDEDEDEDEDEDEDELEVLERK 60
 QY 61 PAAGLSAAAVPAAAPLDDSSDVPPAPRGPLPAAPPAAPROPSKERSPAAAPAPSLP 120
 DB 61 PAAGLSAAAVPAAAPLDDSSDVPPAPRGPLPAAPPAAPROPSKERSPAAAPAPSLP 120
 QY 121 PAAAVLPKLPDEDEPPAPPPPPAGASPLAEPAAPSTPAAPKRRSGS 171
 DB 121 PAAAVLPKLPDEDEPPAPPPPPAGASPLAEPAAPSTPAAPKRRSGSVDLTFALP 180
 QY 172 ----- 171
 DB 181 AASEFVIPSSAEKIMDLMEQFGNTVSSQEDFPVLLLETAASLPSLSTVSKHEGYL 240
 QY 172 ----- 171
 DB 241 GNLGAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSFGKPGKES 300
 QY 172 ----- 171
 DB 301 AILVENTKEEVIVRSKDKEDLVCSAALHSQESPVGKEDRVVSPKTMDFINEMQMSVVA 360
 QY 172 ----- 171
 DB 361 PVREYADFKPQAEWVKDTEGSRDVLAAANVESKVDKRCIEDSLQKSLGKDSGR 420
 QY 172 ----- 171
 DB 421 NEDASFPSTPEPVKDSRAYITCASFTSATESTTANTFPILLEDHTSENKTEKKIEERKA 480
 QY 172 ----- 171
 DB 481 QIITEKTSKPTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTDLVQEAESSEL 540
 QY 172 ----- 171
 DB 541 NEATGKIAYETKVDLVQTSSEAIQESLYPTAQLCPSEAEATPSPVLDPDIMEAPLNSL 600
 QY 172 ----- 171
 DB 601 LPSGASVQVSPSLEAPPVVSIDSKLEPENPPPYEAMNVALKALGTKEGKEPESF 660
 QY 172 ----- 171
 DB 661 NAAVQETEAPYISIACDLIKETLSTEPSPDFSNYSYSEIAKPEKSVPEHAELVEDSSPSE 720
 QY 172 ----- 171
 DB 721 PVDLFSDSDSIPEVPQTQBEAVMLKESLTVSETVAQKKEERLSGASPOELGKPYLESQP 780
 QY 172 ----- 171
 DB 781 NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLLSSKEDKIKESFSDSSPIE 840
 QY 172 ----- 171
 DB 841 IIDEFPTFVSAKDDSPKLAKEYTDLVSDKSEIANIQSGADSLPCLLECDLSPKNIYPK 900
 QY 172 ----- 171
 DB 901 DEVHVSDEFSENRSVSKASISPSNVSALEPQTEGSIKSVKSLTKAEAKKLPSSTEKED 960
 QY 172 -----SVDDLLYWRDIKKTGVVFGASLFLLLSLTIVFSIVSVTAYIALALLS 217
 DB 961 RLSAVALSAELSKTSVDDLLYWRDIKKTGVVFGASLFLLLSLTIVFSIVSVTAYIALALLS 1020
 QY 218 VTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISELVQKYSNLSALGHVNSTIKELRRL 277

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2005, 10:29:31 ; Search time 24.9653 Seconds
(without alignments)
1387.446 Million cell updates/sec

Title: US-09-830-972-2-FUSED

Perfect score: 1823

Sequence: 1 MEDIDQSLVSSSTDSPRP.....VKDAMAKIQAKIPGLKRRAD 360

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.1

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: pir1.*
- 2: pir2.*
- 3: pir3.*
- 4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	826.3	45.3	776	2 A46583	neuroendocrine-spe
2	683	37.5	208	2 I60904	neuroendocrine-spe
3	669	36.7	267	2 A60021	tropomyosin-relate
4	437.7	24.0	2484	2 T26216	hypothetical prote
5	427.4	23.4	2607	2 T28215	hypothetical prote
6	337.5	18.5	222	2 T28213	hypothetical prote
7	272.1	14.9	786	2 A35466	progesterone recep
8	266.9	14.6	1173	2 T31421	C-terminal domain-
9	265.5	14.6	1611	2 T38236	hypothetical prote
10	258.5	14.2	1058	2 T13286	capuccino gene pr
11	257.8	14.1	1100	2 JC8033	leukocyte formin p
12	257.5	14.1	1206	2 S24407	formin isoform IV
13	256.4	14.1	3530	2 A59266	unconventional myo
14	254.9	14.0	1468	2 S11515	formin - mouse
15	254.7	14.0	716	2 T26998	hypothetical prote
16	253.8	13.9	760	2 F86387	probable Pto kinas
17	253.2	13.9	929	2 C96623	hypothetical prote
18	253.2	13.9	1255	2 T13065	diaphanous protein
19	252.2	13.8	2157	2 S71461	proline-rich prote
20	251.9	13.8	1201	2 G86441	unknown protein li
21	250.9	13.8	1015	2 JC6552	DNA topoisomerase
22	250.2	13.7	907	2 E96636	hypothetical prote
23	246.4	13.5	1657	2 T19536	hypothetical prote
24	246	13.5	1522	2 T39371	transcription regu
25	245.8	13.5	645	2 A71416	hypothetical prote
26	245.4	13.5	1460	1 EDBE1F	hypothetical prote
27	245.2	13.5	3511	2 A59295	immediate-early pr
28	245.1	13.4	710	2 D96728	unconventional myo
29	244.7	13.4	465	2 G02738	hypothetical prote
					FRAC-4 - human

30	244.3	13.4	1064	2 T13963	formin related pro
31	242.7	13.3	1533	2 T00344	hypothetical prote
32	242.1	13.3	1375	2 S48375	hypothetical prote
33	241.9	13.3	1213	2 A58198	serine/proline-ric
34	241.7	13.3	3938	2 T42761	Bassoon protein -
35	241.1	13.2	775	1 EDBE11	immediate-early pr
36	240.9	13.2	980	2 G75523	probable cell divi
37	240.6	13.2	1634	2 T28517	hypothetical prote
38	240.5	13.2	1446	1 A45344	immediate-early pr
39	238.9	13.1	731	2 T04455	hypothetical prote
40	238.5	13.1	1047	2 A55617	masquerade precurs
41	238.5	13.1	1420	2 T37781	probable cytoskele
42	238.4	13.1	7962	2 I38346	elastic titin - hu
43	238	13.1	3149	1 QQBE8	BPL1 protein - hu
44	237.6	13.0	933	1 QRHUP	progesterone recep
45	237.5	13.0	980	2 S54986	regulatory protein

ALIGNMENTS

RESULT 1

A46583

neuroendocrine-specific protein, splice form A - human

N:Contains: neuroendocrine-specific protein, splice form B

C:Species: Homo sapiens (man)

C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004

C:Accession: A46583; I60903

R:Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; V&

J. Biol. Chem. 268, 13439-13447, 1993

A:Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spec

A:Reference number: A46583; MUID:93293865; PMID:7685762

A:Accession: A46583

A:Status: preliminary; translated from GB/EMBL/DBBJ

A:Molecule type: mRNA

A:Residues: 1-776 <ROI>

A:Cross-references: UNIPROT:Q16799; GB:I10333; NID:g307306; PIDN:AAAS9950.1; PID:g307307

A:Accession: I60903

A:Status: preliminary; translated from GB/EMBL/DBBJ

A:Molecule type: mRNA

A:Residues: 421-776 <ROE2>

A:Cross-references: GB:I10334; NID:g307308; PIDN:AAAS9951.1; PID:g307309

C:Genetics:

A:Gene: GDB:RTN1; NSP

A:Cross-references: GDB:203968; OMIM:600865

A:Map position: 14q21-14q22

Query Match 45.3%; Score 826.3; DB 2; Length 776;

Best Local Similarity 27.7%; Pred. No. 6.7e-20;

Matches 195; Conservative 52; Mismatches 91; Indels 367; Gaps 17;

QY	10	VSSSTDS-----	PPR-----	19
DB	85	VSSANDHTFSTSKDGECSYLSIDICYPQEDSTYFTGILQKENGHVITSESPEELG	144	
QY	20	PPP-----	AFKQVFTPEP	34
DB	145	TFGPSLPDPVPGIESRGLFSSDSGIEMTPAESTENVKNILADPDQMKAEYKYIDITRPEE	204	
QY	35	EDEDEEDED-----	DED-----	50
DB	205	VKHQSHPELEDKOLDPFKNKDTDISIKPEGVREPKPAPVEGKIHKHLLBESTPAPYI	264	
QY	51	-----	LEEL-----	55
DB	265	DDLSEQRRAPIITTPVKITLIEIPSVETTTQETKPEKQDICKLPSPDTVTVTVSEPE	324	
QY	56	-----	VLERKPAAGLS-----	66
DB	325	DDSPGSIPTPSSGTEPSAAESQKSGISSEDELITAIKEAKGLSYETAENPRPVGLADRP	384	
QY	67	---AAAVPAAAPLLDFSSDSV-----	PPA 89	

[illegible]

RESULT 2
I60904
neuroendocrine-specific protein C - human
C/Species: Homo sapiens (man)
C/Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C/Accession: I60904
R/Receptor: A.J.J. van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; V.
J. Biol. Chem. 268, 13439-13447, 1993
A/Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spe
A/Reference number: A46583; MUID:93293865; PMID:7685762
A/Accession: I60904
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-208 <RES>
A/Cross-references: UNIPROT:Q16799; GB:I10335; NID:G307310; PIDN:AAAS9952.1; PID:G307311
C/Genetics:
A/Gene: GDB:RTN1; NSP
A/Cross-references: GDB:203968; OMIM:600865
A/Map position: 14q21-14q22

Query Match	37.5%	Score 683;	DB 2;	Length 208;
Best Local Similarity	67.4%;	Pred. NO. 1.8e-16;		
Matches 128; Conservative	31;	Mismatches 31;	Indels 0;	Gaps 0;
Qy	171	SSVVDDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIFPRIYKGVIQ	230	
Db	19	SOAIDLLYWRDIKGTIGVFGSFLLLFSLTQFSVVSVVAYIALAALSATISPRIYKSVLQ	78	
Qy	231	AIQKSDGHPPRAYLESEVALSEELVQKYSNALSALGHVNSTIKELRRLFLVDDLVLDSLKFA	290	
Db	79	AVQKTDGHPFKAYLELEITLSQEQIKQYKTCLOQFYVNSTIKELRRLFLVQDLVDSLKFA	138	
Qy	291	VLMWVFYVVGALFNGLTLLIALLSFISPIVYIERHVOQIDHYGLANKSVKDMAKTQA	350	
Db	139	VLMWLLTYVGHALFNGLTLLMAVSMFTLPVVYVKHQAIQOYLGVLVRTHNAVVAKTQA	198	
Qy	351	KIPGLKRRAD	360	
Db	199	KIPGAKRHA	208	

RESULT 3
A60021
tropomyosin-related protein, neuronal - rat
C;Species: Rattus norvegicus (Norway rat)
C;date: 03-Mar-1993 #sequence revision 03-Mar-1993 #text change 05-Nov-1999

C;Accession: A60021
R;Wieczorek, D.F.; Hughes, S.R.
Brain Res. Mol. Brain Res. 10, 33-41, 1991
A;Title: Developmentally regulated cDNA expressed exclusively in neural tissue.
A;Reference number: A60021; MUID:91278684; PMID:1647480
A;Accession: A60021
A;Molecule type: mRNA
A;Residues: 1-267 <WIE>
A;Cross-references: EMBL:X52817; NID:G456549; PIDN:CAA37001.1; PID:G456550
C;Comment: This neuronal-specific mRNA was identified by hybridization to an alpha-tropo-

	Query Match	Score 669;	DB 2;	Length 267;
	Best Local Similarity	66.7%;	Pred. No. 1e-15;	
	Matches 124;	Conservative 32;	Mismatches 30;	Indels 0;
	Gaps 0;			
Qy	171	SSVVDLLYWRDIKKTGVVFGASFLLLLSITVFSIVSVTAIYIALLSVTSFRIYKGVIQ	230	
Db	10	SOATDLYWRDIKGTIGVFGSFLLLFSLTQFSVSVVWAYLALAAALSATISFRIYKSVLG	69	
Qy	231	AIQKSDGHPFRAYLESVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFA	290	
Db	70	AVQKTDGHPFRAYLEITLSQEIQKTYTDCQLQYVNSTLKELRRLFLVQDLVDSLKFA	129	
Qy	291	VLWVFTYVVGALFNGLLTLLIALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIQ	350	
Db	130	VLWMLLYVVGALFNGLLTLLMAVVSMTLPVVYVSKHQVQDQYGLVTRTHINTVVAKIQ	189	
Qy	351	KIPGLK 356		
Db	190	KIPGAR 195		

RESULT 4
T26216
hypothetical protein W06A7.3c - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T26216
R/Ainscough, R.
submitted to the EMBL Data Library, August 1996
A/Reference number: Z20173
A/Accession: T26216
A/Status: preliminary; translated from GB/EMBL/DBDJ
A/Molecule type: DNA
A/Residues: 1-2484 <WIL>
A/Cross-references: UNIPROT:Q9U347; EMBL:Z78066; PIDN:CAB51467.1; GSPDB:GN000023; CESP:W06A7
A/Experimental source: clone W06A7
C/Genetics:
A/Gene: CESP:W06A7.3c
A/Map position: 5
A/Introns: 1827/1; 1866/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2

```

Query Match      24.0%; Score 437.7; DB 2; Length 2484;
Best Local Similarity 14.8%; Pred. NO. 1.5e-05;
Matches 135; Conservative 77; Mismatches 138; Indels 563; Gaps 21;

Qy      1 MEDIDQSSL-----VGSST-----14
          |||::|||
Db      1566 MEVTESEISEMARQVESTCPIPEPLADLKLPEVDEKTPPEPVPGVQVERIPIEV 1625
          |||::|||
Qy      15 -----DSPPRPAPKYQF--VTEPEDE-----35
          |||::|||
Db      1626 EQAPTIFQRPPRAPKSELPKVAKPLDDSKSRVRFAPLNIKLGRTYSEEQKELVESLERP 1685
          |||::|||
Qy      36 -----ED-----EEEEEE-----44
          |||::|||
Db      1686 LTIITQQPPEKPTEDIGALSPLSNTLAEEYEEVPMDMQSVPHSPQEKQEETALSEII 1745
          |||::|||
Qy      45 -----BEDEDLEELVL-----57
          |||::|||
Db      1746 BEPQAMEKEVPBSAPEKNESLEAPIINEPIRRVLVTETKIMGPGKSLNEDNDDDG 1805
          |||::|||
Qy      58 -----57

```

Db 1806 SECLDSIGLSERTIQRFTNTSIDDPSIRRDSPSSISFGDRKFRRTAENIRQDILLPQOS 1865
QY 58 -----DSPRRPPPAKYQF--VTEPEDE-----ERKPAA----- 63
Db 1866 SVSQYLRRSPNPSQQLLVNLSMDSPSLSPNAPPVGFNTAQFLKLEKQEDRPSAEGSI 1925
QY 64 -----GLSAAAVPP-----ED-----EEEBEDE----- 44
Db 1926 DSSGFEKVDHEGLDEFAAPPVHDPMQSVFSGSLGSDMKPGSQDDGFVFIERNANEATL 1985
QY 73 -----AAAAPLL-----BEDDEDLELEVL----- 57
Db 1986 KKNQKMSHHNDVIEKNYFNNDNAPTAALLSPAEARKLVQDAVESAYKKQAVDSDG 2045
QY 80 -----DFSSDSVPPA-----PRGPL 94
Db 2046 EIGRELLDNVEQKIEQVKEPIVDSLHKAYDVGDFVHETVPNAVDDFVREAEKQLPESV 2105
QY 95 P-----AAPP-----AAPP-----ERQ 105
Db 2106 PEKIETPEPLVDIHDVTQKHDEVDNFLRRPTPPFETDDVAPLSDDKPQFGNQTEPEDE 2165
QY 106 PSWER-----SPAAPAPSLPPAAAVLPSKLPEDD 134
Db 2166 TTFDRKGLPTIPEEVEKAAQAQNDLDDFDPLVTSNTGAAGAAVAV--ESLTEEE 2223
QY 135 -----EPAPRPPPPPPAGASPLAEPAPPT-----PAAP-----KRGSG- 170
Db 2224 MFGHQKFETVPRPTPP-----KDISEDVKPSTVNLGSPSHHSHPSHILKHGDGAW 2279
QY 171 -----SSVDLLIWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFR 223
Db 2280 IDFKTVPPCLVDIYWRDAKSAIYLSALLVFLAKYPLLTVTYTSLLALGAAAGFR 2339
QY 224 IYKGVIOAIQKDEGHPFRAYLESVAISEELVQKYSNSALGHVNSTIKELRRLFLVDL 283
Db 2340 VPKVEAQIKKTDSEHPSEILAQDLTLPOEKVHAQADVFEHATCIANKLKKLVFVESP 2399
QY 284 VDSLKFAVLMVFTYVVGALFNGLTLLILALISLPSIPVIYERHQVQIDHYLGLANKSVKD 343
Db 2400 LESIKFGLVLSLTVIASWFSQFTLAILGLGVFSVPKYVESNQEAIDPHLATISGHLKN 2459
QY 344 AMAKTOAKIPGLK 356
Db 2460 VQNIIDEKLPFLR 2472

RESULT 5

hypothetical protein W06A7.3a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26215
R:Ainscough, R.
submitted to the EMBL Data Library, August 1996
A:Reference number: Z20173
A:Accession: T26215
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2607 <WIL>
A:Cross-references: UNIPROT:Q23187; EMBL:Z78086; PIDN:CAB01522.2; GSPDB:GN000023; CESP:W06A7.3a
A:Experimental source: clone W06A7
C:Genetics:
A:Gene: CESP:W06A7.3a
A:Map position: 5
A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2; 2586/2

Query Match

Best Local Similarity 23.4%; Score 427.4; DB 2; Length 2607;
Matches 135; Conservative 78; Mismatches 137; Indels 686; Gaps 21;

QY

1 MEDIDQSSL-----VSSST----- 14

RESULT 6

Db 1566 MEVVTSESISEMAPQVSESTCPPEPLADLKLPVEDDEKTEPEPEPVPGVQVERIPIEV 1625
QY 15 -----DSPPRPPPAKYQF--VTEPEDE-----ERKPAA----- 35
Db 1626 EQAPTIPQPPRAPKSELPAKPLDDSKSRVRFAPLNIKLGRTYSEEQKELVESLERP 1685
QY 36 -----ED-----EEEBEDE----- 44
Db 1686 LTIITQOKPEKPTEDIGALSPLSPNTLAEEVEVPMQSVPHSPQEKQEBIEALSEI 1745
QY 45 -----BEDDEDLELEVL----- 57
Db 1746 BEPQAMKEVEKVESAPKDNESLEAPEIINEPIRRVLVETKIMGFGKSLNEDNDDDDG 1805
QY 58 ----- 57
Db 1806 SECLDSIGLSERTIQRFTNTSIDDPSIRRDSPSSISFGDRKFRRTAENIRQDILLPQOS 1865
QY 58 -----ERKPAA----- 63
Db 1866 SVSQYLRRSPNPSQQLLVNLSMDSPSLSPNAPPVGFNTAQFLKLEKQEDRPSAEGSI 1925
QY 64 -----GLSAAAVPP-----ED-----EEEBEDE----- 72
Db 1926 DSSGFEKVDHEGLDEFAAPPVHDPMQSVFSGSLGSDMKPGSQDDGFVFIERNANEATL 1985
QY 73 -----AAAAPLL----- 79
Db 1986 KKNQKMSHHNDVIEKNYFNNDNAPTAALLSPAEARKLVQDAVESAYKKQAVDSDG 2045
QY 80 -----DFSSDSVPPA-----PRGPL 94
Db 2046 EIGRELLDNVEQKIEQVKEPIVDSLHKAYDVGDFVHETVPNAVDDFVREAEKQLPESV 2105
QY 95 P-----AAPP-----AAPP-----ERQ 105
Db 2106 PEKIETPEPLVDIHDVTQKHDEVDNFLRRPTPPFETDDVAPLSDDKPQFGNQTEPEDE 2165
QY 106 PSWER-----SPAAPAPSLPPAAAVLPSKLPEDD 134
Db 2166 TTFDRKGLPTIPEEVEKAAQAQNDLDDFDPLVTSNTGAAGAAVAV--ESLTEEE 2223
QY 135 -----EPAPRPPPPPPAGASPLAEPAPPT-----PAAP----- 166
Db 2224 MFGHQKFETVPRPTPP-----KDISEDVKPSTVNLGSPSHHSHPSHILKHGDGAW 2279
QY 167 ----- 166
Db 2280 IDFKTVPPCAQNAFSGEIMFLAPFVYLSCFASFKSLPLLDNLLSLVYLSLIIH 2339
QY 167 ----- 166
Db 2340 VKHHRKFRWNEEQATTMSKLGAVGRGLYALIAFVNIVLVGLNVALVGVAVSAEAYK 2399
QY 167 --RGSG-----SSVDLLIWRDIKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTI 220
Db 2400 LTKSSGVLRKKEVLVDIYWRDAKSAIYLSALLVFLAKYPLLTVTYTSLLALGAA 2459
QY 221 SFRIYKGVIOAIQKDEGHPFRAYLESVAISEELVQKYSNSALGHVNSTIKELRRLFLV 280
Db 2460 GFRVFKVEAQIKKTDSEHPSEILAQDLTLPOEKVHAQADVFEHATCIANKLKKLVFV 2519
QY 281 DDLVDSLKFAVLMVFTYVVGALFNGLTLLILALISLPSIPVIYERHQVQIDHYLGLANKS 340
Db 2520 ESPLESINFGVLWSLTVIASWFSQFTLAILGLGVFSVPKYVESNQEAIDPHLATISGH 2579
QY 341 VKDAMAKTOAKIPGLK 356
Db 2580 LKNVQNIIDEKLPFLR 2595

QY 161 PAAP----- 164
DB 358 SAAPPGLYPLGLNGHQALGFAAVALKEGLPOLCPVLYVVRPDTETSSQSQSYFESLP 417
QY 165 -----KR-----RGSGSVVDLL-----Y 178
DB 418 QKILICGDEAGSGHYGVLTGCGSKVFFKRAMEGQHNYLCAGNDCIVDKIRKNCPCACR 477
QY 179 WRDIKKTGVVFGASIFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDG 238
DB 478 LKCCQAGNVLGKRFKLN-----KMKVVRTLDVALQOP--- 512
QY 239 HPFRAYLSEVAISEELVQKYS---NSALGHVNSTIKELR----- 275
DB 513 ----AVLQDE---TQSLTORLSFSPQEIPIFPFPMISVLRGIEPEVYVAGYDNTKPTPS 565
QY 276 -----RLFLVDDLVDSLKFAVLMWVFTYVGVGALFNGLTL 308
DB 566 SLLTSLNLHLCERQLLCVVKWSKLLPGFRNLHIDDQITLQYS---W-----MSL 611
QY 309 LIAL-----ISLFSIPVIYERHQVIDHY 333
DB 612 MVFANGWRSYKHVSGOMLYFAPDLILNEQRMKESFYSLCLSMWQLPQEFVRLQVSYQBEF 671
QY 334 L-----GLANKSVKDM-----AKIQAKIPGLKPK 358
DB 672 LCMKALLLNTIPLGLRSQSFDEMRTSYIRELVKAIGLRQK 714

RESULT 8
T31421
C-terminal domain-binding protein rbl - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31421
R.Yuryev, A.; Patturajan, M.; Litington, Y.; Joshi, R.V.; Gentile, C.; Gebara, M.; Cord
Proc. Natl. Acad. Sci. U.S.A. 93, 6975-6980, 1996
A:Title: The C-terminal domain of the largest subunit of RNA polymerase II interacts with
A:Reference number: Z21024; MUID:96293459; PMID:8692929
A:Accession: T31421
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1173 <YR>
A:Cross-references: UNIPROT:Q63624; EMBL:U49056; NID:g1438531; PID:g1438532; PIDN:AA0526
A:Experimental source: hippocampus

Query Match 14.6%; Score 266.9; DB 2; Length 1173;
Best Local Similarity 9.8%; Pred.No. 1.4;
Matches 116; Conservative 32; Mismatches 69; Indels 961; Gaps 26;

QY 11 SSSDTPSPRPSP-----AF-----KYQ----- 27
DB 119 SSSSPSPSPSPSPPPPPALPAPRFIDYDPFHTDEAYSPPAEQKYDPFEATGNPSS 178
QY 28 -FVTEPEDEEEDDEE----- 45
DB 179 GGTSPSEEEEEEEEGLSQSIRRISETLAGIYDNLSDQDPFGDDSPHREPPPT 238
QY 46 -----EDD 48
DB 239 LGAGTTPQADSTRAEGAPRRRVFVVGPEAEACLEGKVSVEVVTAGGALPLPLPPTD 298
QY 49 EDLEEVLE-----RKP-----AAGLSAAVPPAAA---AP-----LL 79
DB 299 PIEEGEIVQPEERVAVSLFRAAPROPASVATLASVAAPAPASAPAPAGDDFL 358
QY 80 DFSSOS-----VPPAP-----RGPLPAAPPA--- 100
DB 359 SLHADSDEGALQVDLGEPPAPPAADRWGGLDRLKILTORRERYQRKASGPGPPARK 418
QY 101 -----APERQPSWE----- 109

DB 419 KARRERQSGDPAPDPDPTWEAKCHRSRERKLGSHSTARRSRSRSRSRSRSRADRRG 478
QY 110 -----RS-----PAA----- 114
DB 479 SHRSRSRKR 538
QY 115 ---PAPSLP-----PAAV 125
DB 539 EKLPAVPVPPSGDRDRRRRGAVPPSIQDLTHDLFAIKRTITVGRPDKTEPRAPSPAPAV 598
QY 126 LPS----- 128
DB 599 SPKGEVLYDSGLSADERGAOKDKDRRRSGAASSSSSSSSSKASRRKALDGRDRDRSS 658
QY 129 ---KLPEDEP----- 136
DB 659 KKPRTPKDSAPGSGALPKAPRSGSSSSSSSSSSSSSKRVKVLQSKVAVLIREGVSTTPAKDS 718
QY 137 ----- 136
DB 719 SSSGLSIGVKFSDRDRSRPFLKPDERSPAGVKVAFGSKPKPKTKAKAKAGAKAGT 778
QY 137 -----P 137
DB 779 KGKTKPKTRKVRSGSGSTASGGPSLKKSKADSCSOAASAKGTETESWSGEERTTKAP 838
QY 138 ARPP----- 145
DB 839 STPPPKVAPPPPALTPDQTVDSCKTPDVSFSLAEASEDTGVRVGABEEEEEEEEEE 898
QY 146 -----AGASPLAEPAA----- 156
DB 899 EQQPATTTATSTAAPSTAPAGTAGDGAEDGPAARASQLPTLPPMPWNLPAQVD 958
QY 157 -----PPST----- 160
DB 959 CTTSGVLALTALLFKMEANLASRAKAQELIQTNTQILHRKFPSTGLVTPAPVTSFGL 1018
QY 161 -----PAAPKRGSGSSVVDLYWRDIKKTGVVFGA 191
DB 1019 PPAPSYLLPGSLPIGGCGSTPPTGLVPSADKREGSSSS----- 1059
QY 192 SLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLSEVAI 251
DB 1060 -----EGR----- 1062
QY 252 SEELVQYSNAGLGHVNSTIKELRELFLVDLDVLSLKFAVLMWVFTYVGVGALFNGLTL 311
DB 1063 -----GTDKYLKLTQERAVEVK----- 1083
QY 312 ALISLFSIPVIYERHQVIDHYLGLANKSVKADMAKIOAKI----- 352
DB 1084 -----LSIKPVYQKDIKKEEY-----KDLKRAVHKICHKSKEINPVKSNLVRA 1130
QY 353 -----PGL 355
DB 1131 YVQRYRYFRKHGKPGDPPGPPRPKPEGPPDKGGPGL 1168

RESULT 9
T38236
Hypothetical protein SPAC23A1.17 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T38236
R.Murphy, L.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, February 1998
A:Reference number: Z21780
A:Accession: T38236
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1611 <MUR>
A:Cross-references: UNIPROT:O42854; EMBL:AL021813; PIDN:CAAL6991.1; GSPDB:GN00066; SPDB:

A:Experimental source: strain 972h-; cosmid c23A1
C:Genetics:
A:Gene: SPDB:SPAC23A1.17
A:Map position: 1

Query Match 14.6%; Score 265.5; DB 2; Length 1611;
Best Local Similarity 10.1%; Pred. No. 3.4;
Matches 131; Conservative 59; Mismatches 106; Indels 1005; Gaps 30;

```

QY 2 EDIDSSLSVS-----SSTDSPPRP----- 20
D 299 EELSKSQVAKDDDDPVVSNNTANSDEPASSKPAKPLTLNRAFSQRLNLPQPKGKSG 358
QY 21 -----PPAFKYQFVTEPD-----EEDDEEEDDEE 46
D 359 ELSEQDEEYDAESDENHSPSYSTHEPESEFDQDPEKDDENKDVEEQEQEQQEQI 418
QY 47 DDELEELVLEVL----- 59
D 419 DPEEAKRIALRERMAKMGSGGIMHVFGLPLGLAIPGRKNTLRRTPAKSSEAKSTNDSS 478
QY 60 -----KPAAGLS 66
D 479 PKDSSSTQTEQSNQAQAPSPKEERPLPSEFSONQPAEYRDTPTPRNIMPGLM 538
QY 67 AA----- 68
D 539 SADQPIKVTSPNSADKAIVAGPNNEBETKGPVETQETSEQQVHKTPPEKQKVLSP 598
QY 69 -----AVPPAAAPFL----- 79
D 599 PPIITNFKETILASNEAEAVPKDSAPQVTRLMAPODSSSVVTPSPSTLLDPAARVKV 658
QY 80 -----DESS-----DS 85
D 659 IDGIDPPKEAGAGATDVESAANSPIPTPRTWHSDFTSKFEPIERKLPSRISVETDS 718
QY 86 V-----PPAP----- 90
D 719 IDEDKQNEVDSTARSALPPCLGRGKVDTLASLAHDDLDLPAVPRIFSPPLPKTPSG 778
QY 91 -----RG-----P 93
D 779 EFGDNEFMFKSNRVRGHQSRPSTGSQLRNVVPSIVTSGRPLALPDEMASPSSIGHP 838
QY 94 LPAAPPA-----APERQSWERS----- 111
D 839 LPSPPPADFNLSUNDFYEPHYSLESPAPEQPSYEEESFNATVTHAPTSTATFOGHPTI 898
QY 112 ----- 111
D 899 SNVATPPLKQDVTEKASPVADASATHOSSTGLTQETITQLGSNMRLPTKLTSPSNDGRKA 958
QY 112 -----PAAPAPSLPPAAAV-----L 126
D 959 SGPRPAAP-PSIPPLPLPVSNILSSPTSPBKDHPPSAPLSKPVSTSPAALARVPPVKL 1017
QY 127 PSK-----LPEDDEP----- 137
D 1018 SSKAPVFLPSADAPPFVSTAPPVPIPTSTPPVKSSSGAPSPAPPVPAPSSEIPSIP 1077
QY 138 ----- 137
D 1078 APSGAPPVPAGSIPPVKPSVAAPVPVKPSVAAPVPVAPSPGAPPVPKPSVAAPVPVPS 1137
QY 138 -----ARPPPPPPAGASPLAEP--AAPP----- 158
D 1138 GAPPVKPSVAAPVPAPSPAGAPPVKPSVAAPVPVAPSPGAPPVPKPAAGVPVPPVPPSEA 1197
QY 159 -----STP----- 161
D 1198 PPVPKPSGVPPVPPPPSTAPPVFTPSAGLPPFVVPVTKAPVPVAPSPSEASVSTPRSSVP 1257

```

```

QY 162 -----AAPKR-----RGS 169
D 1258 SPHSNAPSPTSSSMASAPARTSVSRSKSKAERHETSTSRKSKSGEHHHHHNEGHAD 1317
QY 170 GSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVF-----SIVSVTAYI----- 211
D 1318 SSSTRTSLAHQDSRK-----SLRHLSRSSRSRASKKPSIVSTTGPFPNESFSKAPVBPFC 1370
QY 212 -----ALALLSVTISFRIYKGV----- 228
D 1371 ASEKWLNLSTAVPKSVQMNDSDVLYMIKEGITGQDKKYKSVHILFPDYSQVTLTATFNPH 1430
QY 229 -----IQAIQKSDGHPFRAYLESEVAISEBELVQK-----YSNKGALGVNSTIKELRLRF 278
D 1431 NQNTQLSQLQALAPQAPSKARLDEEVACYGSTITLKARAYQGSVMVGDSA----- 1481
QY 279 LVDDLVLKFAVLWVFTYVVAL-----FNLTLILLILALISLFSIPVIY 323
D 1482 -----FTFVNSVMSILAHNLEPINKQTFGG-----VIY 1509
QY 324 ERHQVQIDHYLGLANKSVK-----DAMAKIOAKIPGLK 356
D 1510 K-----NVGNVTVQOIGETIRPGDIVTFDKAKFSGQK 1540

```

RESULT 10
T13286
cappuccino gene protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T13286
R:Emmons, S.; Phan, H.; Calley, J.; Chen, W.; James, B.; Manseau, L.
Genes Dev. 9, 2482-2494, 1995
A:Title: Cappuccino, a Drosophila maternal effect gene required for polarity of the egg
A:Reference number: Z17651; MUID:96033799; PMID:7590229
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1058 <EMM>
A:Cross-references: UNIPROT:Q24120; EMBL:U34258; NID:g1061333; PID:g1061334; PIDN:AAC4692
C:Genetics:
A:Gene: capu
A:Cross-references: FlyBase:FBgn0000256

Query Match 14.2%; Score 258.5; DB 2; Length 1058;
Best Local Similarity 16.2%; Pred. No. 2.1;
Matches 114; Conservative 51; Mismatches 103; Indels 435; Gaps 27;

```

QY 4 IDQSSLSVS----- 11
D 340 LESASLASLGGAGVAGSLATATATASSDQKTLQILKRLNLCSTLAEVHAVVNELL 399
QY 12 SSTDSPPRP-----PAFKYQF-----VTEPEDEEEDDEE----- 45
D 400 SSVDEPPRRPCKRCVNLTELLNASEATVYVYKNTGAECVKSFDTAETQETSEDCGCTK 459
QY 46 -----EDDEDLEELVLEKPAAGLSAAVPPAPAAAPLLDFSSSDSVPPAP 90
D 460 CGQSTKVKSNKSAKEDGE-----KPHA---VAPPPPPPPPLPAFVAPPPPPPP 506
QY 91 RGPLP-----AAPPAAPERQPSWERSPAAPAS-----LPPAAAVLPK----- 129
D 507 PPPPPPLANYGAPPPPPPPPGSGSAPPPPPPPAPTEGGGGIPPPPPPMASPSKTTISPA 566
QY 130 -LPEDDE-----PP-----ARPPPPPP-----AG 147
D 567 PLDPPAEGNWFHRTNTRKSAVNPKMRPLYWTRIVTSAPPAPRPPSVANSTDSTENG 626
QY 148 ASPLAEP-----APPSTPAAPKRGSGSSVVDLLYWRDIKKT----- 185
D 627 SSPDEPPAANGADAPPTAPPATKE-----IWTETPLDNIDETFLFSRQAI 675
QY 186 -----GVVFGASLFLLLSLTVFSIVSVTAYIALALLS 217

```


QY 229 IQAIQKSGHP-----FRAYLESEVAISELVQ----- 257
Db 777 IQINDKSQAATLWDSLEEPHRTSEFYLFSDTQOKKKPLSEAYEKKYKXIK 836
QY 258 -----KYNSA-----LGHVNSTIKELRR-LFLVDDLVSLKFAVLMVFTYVGFALFNGLTLL 309
Db 837 LLDGRSQTGVLISLSLHLEMDIQQAFTVDD----- 869
QY 310 ILALISLSIPVIYERHQVIDHYLGLANKSVKDAMAKIQ----- 349
Db 870 --SVVDLETALAYE-----NRAQEDBLTKIRKYETSKEEDLKLDKPEQF 914
QY 350 ----AKIPGLKRKA 359
Db 915 LHELAQINFAERA 928

RESULT 13
A59266
Unconventional myosin-15 - human
C:Species: Homo sapiens (man)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C:Accession: A59266
R:Liang, Y.; Wang, A.; Belyantseva, I.A.; Anderson, D.W.; Probst, F.J.; Barber, T.D.; Mil
an, T.B.; Fridell, R.A.
Genomics 61, 243-258, 1999
A:Title: Characterization of the human and mouse unconventional myosin XV genes responsi
A:Reference number: A59266; MUID:20021762; PMID:10552926
A:Accession: A59266
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-3530 <L1A>
A:Cross-references: UNIPROT:Q9UKN7; GB:AF144094; NID:G6224682; PIDN:NAF05903.1; PID:G622
F:1225-1887/Domain: myosin motor domain homology <MMO>

Query Match 14.1%; Score 256.4; DB 2; Length 3530;
Best Local Similarity 10.1%; Pred. No. 48;
Matches 145; Conservative 54; Mismatches 124; Indels 1106; Gaps 37;

QY 17 PRRPP-----PAFKQFV-----TEPEDEDEEE----- 40
Db 394 PEEVYFYPEESASAFVYPMVPPPIPSPHNPYAHAMDDIAELEEDPADGVERQGTSLRLP 453
QY 41 -----EEDDE 45
Db 454 SAAPEQQMDKPARSKSLIRKFLRPRQVKLFGEKLEVLPPSLDIPILGDADDEE 513
QY 46 EDEDELEVL----- 57
Db 514 EDEELPPVSAVPYGHFPWFGLTPQRNLQALSFAFGHRLGFGFGRPVPRPATSLA 573
QY 58 -----ERKPAAGL----- 65
Db 574 RFLKTLSEKFIARLRGSKTRAGGAPVREAAKYRFGYKLAGMDPEKPGTPIVLRRAQP 633
QY 66 ----- 65
Db 634 RARSSNDARRPAPQAPARTLSHWSALLSPVPPRPPSSGPPAPPPLSPALSGLPRPASP 693
QY 66 -----SAAAVPPAAA----- 76
Db 694 YGSLRRHPPMAAPAHVPPAPQASGAWFVEPPAVSPVPPDLLAFPPGPRFGRGRRGA 753
QY 77 -----PLIDFSSDSVPPAPR-----GPL--PAAPP 99
Db 754 AFGFGASPRASRRRAWSPLASQPSLSRSSPGLGYCSPLAPSPQLSLRTGCFQFPFFLPP 813
QY 100 A-----APERQ-----PSWERSPAAPAPSLPP-----AAAVLPSKL----- 130
Db 814 ARRPSLQESAPRAAGLGPGLGSPPLGCHSPRSSNLPSRLPHTWR 873
QY 131 -----PEDDE----- 135

Db 874 RLSEBPTTRAVPQVRLPFRPPRAGAWRAPLEHRESPREPDSSETPTWTVPPLAPSDVDM 933
QY 136 -PPARPPPPPPAGA-----SPLAEPAAP----- 157
Db 934 PPTQPPSPFWGAGSGRRGFRPPVPENPFLQLGLPVSPPTLOPEDPAADMTWVFLGRH 993
QY 158 -----PSTPAAPK----- 165
Db 994 HEPGQQLTKSAGTPKPEBEENLGDQLPAETKPTTPAPPKQVTPPKDITPPKDVLP 1053
QY 166 -----RR----- 167
Db 1054 QKTLRPSLSYPLAACDQTRATWPPHWRGTLPQAAAPLAPIRAPEPLPKGERRQAPGR 1113
QY 168 ----- 167
Db 1114 FAVVMPRVKLSFQFVGFPATLKQVQPIQDPKPRACSLRWSCLWLRLADAYGMPVRVHT 1173
QY 168 -----GSGSS-----VVDLLYWRDI 182
Db 1174 PQSCHLGPAAACLSLRSWEVGPSPWKNKHSIRNLSMRFRQHGEGVEDMTQLEDL 1233
QY 183 KKTGVVFGASLFLLSLTVFSIVSVT-----AYIALALLSVT--ISFRIY----- 225
Db 1234 QBT-----TVLSNLKIRFERNLITYTIGSILSVNPNFYQMGFIVGPPEQVQY 1279
QY 226 -----K 226
Db 1280 NGRALGENPPLFAVANLAFAMLDKQNCQIIISGESGSGKTEATKLILRYLAAMNQK 1339
QY 227 GVIOAIQ-----KSDGHPFRAYLE-----SEVAISEELVOK-- 258
Db 1340 EVMQIKILEATPLLESFGNAKTVRNDNSRFGKFEVLEFEGGVISGAITSQYLLEKSRI 1399
QY 259 -----YNSNA----- 263
Db 1400 VFOAKNERNYHIFYELLAGLPAQLRQAFSLQEAETYYLNOGNCIEAGKSDADDFFRL 1459
QY 264 -----LGH----- 266
Db 1460 AAMEVLGSPESDQSIIFRILASILHLGNVYFEKYTEDAQEVAASVVSAREIOAVALLOIS 1519
QY 267 -----VNSTIKELRRLF-----LVD--DLVDSLKFVLM--WVFTYVGL-- 302
Db 1520 PEGLKAITFKVTETMR--KIFTLTVESAVDARDAAKLYALLFSLITRVNALLVP 1577
QY 303 -----FNGLTLLIL-----ALISLSIPVI-----YERHQVQ-- 329
Db 1578 RQDTLSIALDIYGFEDLSFNSFEQLCINANENLQYLFNKIVFOEQEYIREQIDWQE 1637
QY 330 ----- 329
Db 1638 ITFADNQRINLISLKPYGILRLDQCCFPQATDHTFLQKHVHHGANPLYSKPMPLP 1697
QY 330 ---IDHYLGLA----- 337
Db 1698 EFTIKHAGKTYQVHKFLDKNHDQVRQDVLDFVRSSTRVVAHLFSSHAQAPQRLGK 1757
QY 338 -----NKSVKDAMAKIQ-----AKIPGL 355
Db 1758 SSSVTRLYKAHTVAAKFOQSLDLVERMERCNPLFMRLCKPNHKEPGL 1806

RESULT 14

S11515

formin - mouse

C:Species: Mus musculus (house mouse)

C:Date: 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C:Accession: S11515

R:Woyschik, R.P.; Maas, R.L.; Zeller, R.; Vogt, T.F.; Leder, P.

Nature 346, 850-853, 1990

A:Title: 'Formins': proteins deduced from the alternative transcripts of the limb deform

A:Reference number: S11515; MUID:90363291; PMID:2392150

A:Accession: S11515

A:Molecule type: mRNA

A:Residues: 1-1468 <W>

A:Cross-references: UNIPROT:Q05860; EMBL:X53599; NID:g52877; PIDN:CAA37668.1; PID:g52878

Query Match 14.0%; Score 254.9; DB 2; Length 1468;
Best Local Similarity 14.5%; Pred. No. 6.3; Indels 431; Gaps 23;
Matches 97; Conservative 40; Mismatches 103;

```
QY 2 EDIDSSVSSSTDSPPRP--PPA-----PKYQ----- 27
D 602 ERASEKGLGPEKITAPPQHQLPPIGASEGFCDFKQTAQKLPNGDGGVWVPGYRGP 661
QY 28 --FVTEPEDEDEEE--EDED-- 48
D 662 CPFLLEKEKTSRSELYLDLPDQSPTEQDDRTQRLQAVWPPPKTKDTEKVGKLYTE 721
QY 49 -----EDLEELEVLER----- 59
D 722 ABYQAAIHLKREHKEEITLQAFELKTFHIRGEHALVTABEAIENLKQOLEKRREG 781
QY 60 -----KPAAGLSAAA----- 69
D 782 CEEMRDVCISTDCCSPKAFRNVCIQTDRETLKPCDAESKATRSQIVPKKLTISLTQL 841
QY 70 -----VPPAAAAPLLDFSSDVSPPAP-----R 91
D 842 SPSKSDKIHPFQREGTSSSSQKISPPAPPTPLPPL-----IPPPPLPPGL 894
QY 92 GLPAAPPAPEQSWERSPAAPSPAPLPPAAVLPKLPEDDEPPARPPPP----- 145
D 895 GLPPAPPPIPV-----CPVSPPPPPPPPP-----PTVPVPSDGGPPPPPPPLPNVLA 944
QY 146 --AGASP-----LAPPAAP-----PSTPAAPKRRGSGS 171
D 945 LPNSGGPPPPPPPPPPGLAPPPGLSFGLSSSSSQVPRKPAIEPSCMPK----- 997
QY 172 SVVDLLYWRDIKKTGVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 231
D 998 -----LYWTR-----IQI 1005
QY 232 IQSDEGHP-----FRAYLSEVAISELVQ----- 257
D 1006 NDKSQDAAPTLDLSLEPHIRDTSEFYLFSDTQKKKPLSEAYEKKNVKYIKLLD 1065
QY 258 -KYNSA--LGHVNSTIKELAR-LFLVDDLDVSLKFVLMVFTVVGALFNGLTLLILA 312
D 1066 GRSQTVGLISLHLEMKDIOQAFTVDD-----S 1096
QY 313 LISLFSIPVIYERHQVIDHYLGLANKSVKDAWKIQ----- 349
D 1097 VVDLETALAYE-----NRAQEDLTIRKYVETSKEEDLKLDDKPEQFLHE 1143
QY 350 -AKIFGLKKA 359
D 1144 LAQIPNFAERA 1154
```

RESULT 15

T26998

hypothetical protein Y48B6A.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T26998

R:Wall, M.

submitted to the EMBL Data Library, September 1999

A:Reference number: Z20297

A:Accession: T26998

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-716 <WIL>

A:Cross-references: UNIPROT:Q9U2A6; EMBL:AL110490; NID:e1542263; PIDN:CAB54442.1; CESP:X

A:Experimental source: clone Y48B6A

C:Genetics:

A:Gene: CESP:Y48B6A.6

A:Introns: 38/3; 196/3; 437/2; 460/3; 518/1; 617/3; 673/3

Query Match 14.0%; Score 254.7; DB 2; Length 716;
Best Local Similarity 16.9%; Pred. No. 1.1; Indels 353; Gaps 23;
Matches 101; Conservative 39; Mismatches 39;

```
QY 5 DOSSLVSSSTD-----SPRRPP-----PAKQYQVFTPEDEDEDEEED 48
D 178 EMESLVQKQVDVLDQIMSSPPPPPTSPQLPPTPARITSVRSDESIEEERRRKESET 237
QY 49 EDLELEV-----LEKPPAAGLSAAAAPPAAAPLLDFSSDVSPPAPRGGLP----- 95
D 238 ASFELEAEIMRISRP-----VPP-----PVL-----SIPPPPPNIPPLTIPQEVQSP 282
QY 96 -----AAPPAAPERQPSWE-----RSPAAAPAPSLPP----- 121
D 283 PSRPTSVPPPIPPSPGSEDVNMDELIESFSDSVFNNSMSPPLPLPPLRESSELTLEV 342
QY 122 -----AAAVLPKLP-----DDEPPA----- 138
D 343 PEDPVTESKVEASPTPLPKATESLNESSIKALEGLEVKALEAQEASDDRPSAPTPIRDSS 402
QY 139 RPPPPPPAGASPLA-----BPAAP-----PSTPAAPKRR 167
D 403 LPPPPPPKPTPLAIRRAGPIPTPOLLEMIHOEDCSIRPSSPTSVSHGSRQSPAPVKKP 462
QY 168 GSGSSVVDLLYWRDIKKTGVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS----- 221
D 463 -----SVTVSPGLGLC 473
QY 222 -----FRIYKGVIOAI- 232
D 474 DPNLSIEKPEEMKTEDTKPVETAPAPVDEALNDALDRNKINEATCLTKIFPSLVSKYF 533
QY 233 -----QKSDGHP-----PRAYLESE----- 248
D 534 QNCSFDLNDKRSNGENVPLKNNKISLYAESEFSESRKQIQYFSGIFKYYDEQDSYIDFN 593
QY 249 -----VAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDLDVSLKFAVLM 293
D 594 ELKRMMEKLGAEQTHIAL-KELIKKVEDDQDKISQ-----REFFLIFRLAASGE----- 642
QY 294 WVFTYVGALFNGLTLLILALISLFSIPVIYERHQVIDHYLGLANKSVKDAWAKIOAKI 352
D 643 -----LSCSEVFK--TLAESVDVSKEGVLGAAN-----FTQAKI 674
```

Search completed: June 23, 2005, 10:56:54

Job time : 32.9653 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2005, 10:17:56 ; Search time 113.842 Seconds
(without alignments)
1619.338 Million cell updates/sec

Title: US-09-830-972-2-FUSED

Perfect score: 1823

Sequence: 1 MEDIDQSLVSSSTDSPPRP.....VKDAMAKIOAKIPGLKRRAD 360

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.1

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1732.7	95.0	1163	1 RTN4 RAT	Q9JK11 rattus norv
2	1721.6	94.4	356	2 Q8BH78	Q8BH78 mus musculu
3	1712.7	93.9	375	2 Q8BHF5	Q8BHF5 mus musculu
4	1711.5	93.9	357	2 Q8K3G7	Q8K3G7 mus musculu
5	1637	89.8	1162	2 Q8BGM9	Q8BGM9 mus musculu
6	1622.9	89.0	1163	2 Q8K3G8	Q8K3G8 mus musculu
7	1598.4	87.7	392	2 Q9EB16	Q9EB16 homo sapien
8	1518.4	83.3	1192	1 RTN4 HUMAN	Q9NGC3 homo sapien
9	1471.5	80.7	343	2 Q6TPN0	Q6TPN0 homo sapien
10	1012.1	55.5	986	2 Q8TUA4	Q8TUA4 homo sapien
11	1010.2	55.4	1046	2 Q8BQK7	Q8BQK7 mus musculu
12	992.2	54.4	578	2 Q8QW95	Q8QW95 mus musculu
13	988.7	54.2	639	2 Q8K290	Q8K290 mus musculu
14	960.5	52.7	658	2 Q6RSS8	Q6RSS8 gallus gall
15	914	50.1	199	1 RTN4 MOUSE	Q9P972 mus musculu
16	904	49.6	199	2 Q7YRW9	Q7YRW9 bos taurus
17	900	49.4	199	2 Q6IM70	Q6IM70 sus scrofa
18	899.1	49.3	315	2 Q61FY4	Q61FY4 xenopus lae
19	896	49.1	187	2 Q6IG15	Q6IG15 sus scrofa
20	895	49.1	199	2 Q7PCJ7	Q7PCJ7 macaca fasc
21	886.4	48.6	1024	2 Q6JRV2	Q6JRV2 xenopus lae
22	884.5	48.5	1032	2 Q6JRV0	Q6JRV0 xenopus lae
23	883.8	48.5	1032	2 Q6JRV7	Q6JRV7 xenopus lae
24	883.3	48.5	1055	2 Q6JRV1	Q6JRV1 xenopus lae
25	882.2	48.4	330	2 Q6JRV4	Q6JRV4 xenopus lae
26	880.8	48.3	1044	2 Q6JRV8	Q6JRV8 xenopus lae
27	880.5	48.3	311	2 Q6JRV3	Q6JRV3 xenopus lae
28	878.7	48.2	1013	2 Q6JRV9	Q6JRV9 xenopus lae
29	874.8	48.0	199	2 Q7T224	Q7T224 gallus gall
30	870.4	47.7	304	2 Q6JRW0	Q6JRW0 xenopus lae
31	870.3	47.7	323	2 Q6JRW1	Q6JRW1 xenopus lae

RESULT 1

ID	RTN4 RAT	STANDARD;	PRT; 1163 AA.
AC	Q9JK11; Q9JK10; Q9ROD9; Q9WUE9; Q9WUFO;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)		
DE	(Glut4 vesicle 20 kDa protein).		
GN	Name=Rtn4; Synonyms=Nogo;		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.		
RC	STRAIN=Sprague-Dawley; TISSUE=Adipocyte;		
RX	MEDLINE=99249816; PubMed=10231557; DOI=10.1016/S0167-4889(99)00033-6;		
RA	Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lienhard G.E.;		
RT	"Cloning and characterization of a 22 kDa protein from rat adipocytes: a new member of the reticulon family.";		
RL	Biochim. Biophys. Acta 1450:68-76(1999).		
RN	[2]		
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).		
RX	MEDLINE=20129258; PubMed=10667796; DOI=10.1038/35000219;		
RA	Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,		
RA	Spillmann A.A., Christ F., Schwab M.E.;		
RT	"Nogo-A is a myelin-associated neurite outgrowth inhibitor and an		
RT	antigen for monoclonal antibody IN-1.";		
RL	Nature 403:434-439(2000).		
RN	[3]		
RP	SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).		
RC	STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;		
RA	Ito T., Schwartz S.M.;		
RT	"Cloning of a member of the reticulon gene family in rat: one of two		
RT	minor splice variants.";		
RL	Submitted (Feb-1999) to the EMBL/GenBank/DBJ databases.		
RN	[4]		
RP	FUNCTION.		
RX	MEDLINE=20033691; PubMed=12037567; DOI=10.1038/417547a;		
RA	GrandPre T., Li S., Strittmatter S.M.;		
RT	"Nogo-66 receptor antagonist peptide promotes axonal regeneration.";		
RL	Nature 417:547-551(2002).		
CC	-!- FUNCTION: Potent neurite outgrowth inhibitor which may also help		
CC	block the regeneration of the nervous central system in adults (By		
CC	similarity).		
CC	-!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By		
CC	similarity).		
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the		
CC	membrane of the endoplasmic reticulum through 2 putative		
CC	transmembrane domains (By similarity).		
CC	-!- ALTERNATIVE PRODUCTS:		
CC	Event=Alternative splicing; Named isoforms=4;		
CC	Name=1; Synonyms=Nogo-A, NI-220-250;		

32	861.2	47.2	316	2	Q6JRW2	Q6JRW2 xenopus lae
33	855.6	46.9	720	2	Q7TNB7	Q7TNB7 mus musculu
34	844	46.3	179	2	Q9GM33	Q9GM33 macaca fasc
35	826.3	45.3	776	1	RTN1 HUMAN	Q16799 homo sapien
36	826.2	45.3	780	2	Q8K0T0	Q8K0T0 mus musculu
37	823.2	45.2	780	2	Q8K4S4	Q8K4S4 mus musculu
38	807.4	44.3	777	1	RTN1 RAT	Q64548 rattus norv
39	793.9	43.5	760	2	Q90638	Q90638 gallus gall
40	773	42.4	193	2	Q6IFY5	Q6IFY5 xenopus tro
41	766.1	42.0	199	2	Q6PB23	Q6PB23 xenopus lae
42	761	41.7	193	2	Q6JRV6	Q6JRV6 xenopus lae
43	746.1	40.9	199	2	Q6JRW3	Q6JRW3 xenopus lae
44	744	40.8	193	2	Q6JRW4	Q6JRW4 xenopus lae
45	736.6	40.4	214	2	Q7T222	Q7T222 carassius a

<hr/>					
NCBI_TaxID=10090;					
OX	[1]				
RN	SEQUENCE FROM N.A.				
RP	STRAIN=129/SvcJ7; and 129SVCJ7;				
RC	MEDLINE=22376540; PubMed=1248097; DOI=10.1016/S0022-2836(02)01179-8;				
RX	Oertle T., Huber C., van der Putten H., Schwab M.E.;				
RA	"Genomic structure and functional characterisation of the promoters of				
RT	human and mouse nogo/rtn4."				
RL	J. Mol. Biol. 325:299-323(2003).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=129/SvcJ7;				
RA	Van der Putten H.;				
RL	Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=129SVCJ7;				
RA	van der Putten H., Mir A.;				
RL	Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.				
DR	EMBL; AY102284; AM73506.1; -				
DR	EMBL; AY102286; AM73511.1; -				
DR	MGD; MGI:1915835; Rtn4.				
DR	GO; GO:0005783; C:endoplasmic reticulum; IDA.				
DR	GO; GO:0005515; F:protein binding; IPI.				
DR	GO; GO:0001525; P:angiogenesis; IMP.				
DR	GO; GO:0007399; P:neurogenesis; IDA.				
DR	InterPro; IPR003388; Reticulon.				
DR	Pfam; PF02453; Reticulon.1				
DR	PROSITE; PS50845; RETICULON.1.				
SQ	SEQUENCE 1162 AA; 126612 MW; 855697PBBE11781F CRC64;				
Query Match 89.8%; Score 1637; DB 2; Length 1162;					
Best Local Similarity 29.8%; Pred. No. 1.6e-44;					
Matches 348; Conservative 2; Mismatches 6; Indels 810; Gaps 4					
QY	1 MEDIDSSLVSSSTDSPRRPPAFKQVFTPEDEDEDEDEDEDEDEDEDEDEDELEEVLERK	60			
DB	1 MEDIDSSLVSSADSPPRRPPAFKQVFTPEDEDEDEDEDEDEDEDEDEDEDELEEVLERK	59			
QY	61 PAAGLSAAAVPPAAAAAPLLDFSSDSDVPAPRGPLPAAPAAPERQPSWERSPAAPASLP	120			
DB	60 PAAGLSAAVPPP-AAAPLLDFSSDSDVPAPRGPLPAAPTAPERQPSWERSPAASAPSLP	118			
QY	121 PAAVLPSKLPEDEPPAPPPPPAGASPLAEPAAPSTPAAPKRGSGSVVDLLYWR	180			
DB	119 PAAVLPSKLPEDEPPAR--PPAPAGASPLAEPAAPSTPAAPKRGSGSVVDLLYWR	176			
QY	181 DIKKTGW-FGASLFLLSLTVFSIVSVTAYIALALLSVTSIFRYKGVIQAIQKSDEGH	239			
DB	177 DIKKTGWFGASLFLLSLTVFSIVSVTAYIALALLSVTSIFRYKGVIQAIQKSDEGH	236			
QY	240 PFRAYLESEVAISEELVKYSNSALGHVNSTIKELRRLFLVDLDVSLKFVLMVFYV	299			
DB	237 PFRAYLESEVAISEELVKYSNSALGHVNSTIKELRRLFLVDLDVSLKFVLMVFYV	296			
QY	300 GALFNGLTLILALISLFSIPVIYERHQVIDHYHGLANKSVKDAMAKIQIKGLKRKA	359			
DB	297 GALFNGLTLILALISLFSIPVIYERHQVIDHYHGLANKSVKDAMAKIQIKGLKRKA	356			
QY	360 D 360				
DB	357 E 357				
<hr/>					
RESULT 5					
Q8BGM9 Q8BGM9 PRELIMINARY; PRT; 1162 AA.					
ID	Q8BGM9				
AC	Q8BGM9;				
DT	01-MAR-2003 (TEMBLrel. 23, Created)				
DT	01-MAR-2003 (TEMBLrel. 23, Last sequence update)				
DT	05-JUL-2004 (TEMBLrel. 27, Last annotation update)				
DE	Rtn4.				
GN	Name=Rtn4;				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BALB/c;				
RA	Jin W., Li R., Long M., Shen J., Ju G.;				
RL	Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.				
DR	EMBL; AY114153; AM77069.1; -				
DR	MGD; MGI:1915835; Rtn4.				
DR	GO; GO:0005783; C:endoplasmic reticulum; IEA.				
DR	InterPro; IPR003388; Reticulon.				
DR	Pfam; PF02453; Reticulon.1.				
DR	PROSITE; PS50845; RETICULON.1.				
SQ	SEQUENCE 357 AA; 38566 MW; 73BB3DI7DFDBDF15 CRC64;				
Query Match 93.9%; Score 1711.5; DB 2; Length 357;					
Best Local Similarity 96.1%; Pred. No. 3.5e-48;					
Matches 347; Conservative 2; Mismatches 7; Indels 5; Gaps 4;					
QY	1 MEDIDSSLVSSSTDSPRRPPAFKQVFTPEDEDEDEDEDEDEDEDEDEDEDELEEVLERK	60			
DB	1 MEDIDSSLVSSADSPPRRPPAFKQVFTPEDEDEDEDEDEDEDEDEDEDEDELEEVLERK	59			
QY	61 PAAGLSAAVPPAAAAAPLLDFSSDSDVPAPRGPLPAAPAAPERQPSWERSPAAPASLP	120			
DB	60 PAAGLSAAVPPP-AAAPLLDFSSDSDVPAPRGPLPAAPTAPERQPSWERSPAASAPSLP	118			
QY	121 PAAVLPSKLPEDEPPAPPPPPAGASPLAEPAAPSTPAAPKRGSGSVVDLLYWR	180			
DB	119 PAAVLPSKLPEDEPPAR--PPAPAGASPLAEPAAPSTPAAPKRGSGSVVDLLYWR	176			
QY	181 DIKKTGW-FGASLFLL				

537	DB	CESELNEATGKTIAETKVDLVQTSSEAIQESIYPTAOLCPSFEAEATPSPVLPIVMEA	596
172	QY	-----	171
597	DB	PLNSLLPSTGASVAQPSASPLEVSPSVYDGIKLEPNPPPYEEAMSVALKTSDSKBEIK	656
172	QY	-----	171
657	DB	EPESFNAAQAEAPYISACDLIKETKLTSTPSPFESNYSEIAKFKSVDPDHCELVDDS	716
172	QY	-----	171
717	DB	SPSEPVDLFSDDSIPEVPQTOBEAVMLKESLTVSESTVQHKHKERLSASPOEVGKPY	776
172	QY	-----	171
777	DB	LESFQPNLHITKDAASNEIPTLTTKETISLQMBEENFNTAIYNSDDLLSSKEDMKSESTFS	836
172	QY	-----	171
837	DB	DSSPIEIIDFPTFVSADKSPKEYTDLVSNKSEIANVQSGANSLPCSELPCDLSFKNT	896
172	QY	-----	171
897	DB	YPKDEAHVSDPFSKRSRVSXVPLLLPNVSALBSQIEMGNIVPKVLTKEABEKLPSDTE	956
172	QY	-----SVVDDLLYMRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALA	214
957	DB	KEBRSLTAVLSAELNKTSSVDDLLYMRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALA	1016
215	QY	LLSVTISFRIYKGVIOAIQKSDGEGHPRAYLESEVAISEELVQKYSNSALGHVNSTIKEL	274
1017	DB	LLSVTISFRIYKGVIOAIQKSDGEGHPRAYLESEVAISEELVQKYSNSALGHVNSTIKEL	1076
275	QY	RRFLPLVDDLDVLSKFAVLMMVFTVVGALFNGLTLLIALLSLSPYIVYERHVOQIDHYL	334
1077	DB	RRFLPLVDDLDVLSKFAVLMMVFTVVGALFNGLTLLIALLSLSPYIVYERHVOQIDHYL	1136
335	QY	GLANKSVKDAWAKIOAKIPGLKRAKD	360
1137	DB	GLANKSVKDAWAKIOAKIPGLKRAE	1162

RESULT 6

ID	Q9K3G8	PRELIMINARY;	PRT; 1163 AA.
AC	Q9K3G8;		
DT	01-OCT-2002	(T-EMBLrel. 22, Created)	
DT	01-OCT-2002	(T-EMBLrel. 22, Last sequence update)	
DT	01-MAR-2004	(T-EMBLrel. 26, Last annotation update)	
DE	MoGo-A.		
DN	Name=Rtn4;		
GN	Mus musculus (Mouse).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BALB/c;		
RA	Jin W., Long M., Li R., Ju G.;		
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY114152; AA077068.1; -;		
DR	MGD; MGI:1915835; Rtn4.		
DR	GO; GO:0005783; C:endoplasmic reticulum; IEA.		
DR	InterPro; IPR003388; Reticulon.		
DR	Kfam; PF02453; Reticulon; 1.		
DR	PROSITE; PS00845; RETICULON; 1.		
DR	SEQUENCE 1163 AA; 126690 MW; 6B5F362799417EA4 CRC64;		

[illegible]

RN [5] SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
 RP TISSUE=Placenta, and Skeletal muscle;
 RC Ito T., Schwartz S.M.;
 RA "Cloning of a member of the reticulon gene family in human.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Fibroblast;
 RA Yutsudo M.;
 RL "Isolation of a cell death-inducing gene.";
 RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC TISSUE=Embryonic;
 RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,
 RA Luo B., Hu R., Chen J.;
 RL "Human neuroendocrine-specific protein C (NSP) homolog gene.";
 RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
 RA Qin W.X., Huang Y., Qiu X.K., Qian L.P., He L.P., Li H.N., Yu Y.,
 RA Yu J., Han L.H.;
 RL "Novel human cDNA clones with function of inhibiting cancer cell
 growth.";
 RT Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=99156230; PubMed=10048485;
 RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirose M.,
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
 RL "Prediction of the coding sequences of unidentified human genes. XII.
 RT The complete sequences of 100 new cDNA clones from brain which code
 for large proteins in vitro.";
 RL DNA Res. 5:355-364(1998).
 RN [10]
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
 RC TISSUE=Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins B., Wagner L., Shenman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marudina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Touchman J.W., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RL "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [11]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC TISSUE=Umbilical cord blood;
 RX MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200;
 RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
 RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
 RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;
 RL "Cloning and functional analysis of cDNAs with open reading frames for
 300 previously undefined genes expressed in CD34+ hematopoietic
 stem/progenitor cells.";
 RL Genome Res. 10:1546-1560(2000).
 RN [12]
 RP SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).
 RC TISSUE=Brain;
 RA Mao Y.M., Xie Y., Zheng Z.H.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [13]
 RP SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1).
 RC TISSUE=Testis;
 RA Sha J.H., Zhou Z.M., Li J.M.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [14]
 RP TOPOLOGY.
 RC TISSUE=Brain;
 RX MEDLINE=20129259; PubMed=10667797; DOI=10.1038/35000226;
 RA GrandPré T., Nakamura F., Vartanian T., Strittmatter S.M.;
 RL "Identification of the Nogo inhibitor of axon regeneration as a
 Reticulon protein.";
 RL Nature 403:439-444(2000).
 RN [15]
 RP FUNCTION.
 RC TISSUE=Brain;
 RX MEDLINE=21069055; PubMed=11201742; DOI=10.1038/35053072;
 RA Fournier A.E., Grandpré T., Strittmatter S.M.;
 RL "Identification of a receptor mediating Nogo-66 inhibition of axonal
 regeneration.";
 RL Nature 409:341-346(2001).
 RN [16]
 RP REVIEW.
 RC MEDLINE=2188956; PubMed=11891768; DOI=10.1002/jnr.10134;
 RA Ng C.E.L., Tang B.L.;
 RL "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron
 regeneration.";
 RL J. Neurosci. Res. 67:559-565(2002).
 CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
 CC block the regeneration of the nervous central system in adults.
 CC Isoform 2 reduces the anti-apoptotic activity of Bcl-xL and Bcl-2.
 CC This is likely consecutive to their change in subcellular
 CC location, from the mitochondria to the endoplasmic reticulum,
 CC after binding and sequestration.
 CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xL and Bcl-2.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum. Anchored to the membrane of the endoplasmic reticulum
 CC through 2 putative transmembrane domains.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=4;
 CC Name=1; Synonyms=RTN 4A, Nogo-A, RTN-XL;
 CC IsoId=Q9NQC3-1; Sequence=Displayed;
 CC Name=2; Synonyms=RTN 4B, Nogo-B, RTN-XS, Foccen-M;
 CC IsoId=Q9NQC3-2; Sequence=VSP_005655;
 CC Name=3; Synonyms=RTN 4C, Nogo-C, Foccen-S;
 CC IsoId=Q9NQC3-3; Sequence=VSP_005652, VSP_005653;
 CC Name=4;
 CC IsoId=Q9NQC3-4; Sequence=VSP_005654;
 CC -!- TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain
 CC and testis and weakly in heart and skeletal muscle. Isoform 2 is
 CC widely expressed excepted for the liver. Isoform 3 is expressed in
 CC brain, skeletal muscle and adipocytes. Isoform 4 is testis-
 CC specific.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -!- CAUTION: Ref.11 sequence differs from that shown due to
 CC frameshifts in positions 1149 and 1156.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AJ251383; CAB99248.1; -;
 DR EMBL; AJ251384; CAB99249.1; -;
 DR EMBL; AJ251385; CAB99250.1; -;
 DR EMBL; AB040462; BAB18927.1; -;


```
Q8BGK7
ID Q8BGK7 PRELIMINARY; PRT; 1046 AA.
AC Q8BGK7;
DT 01-WAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE RTN4.
GN Name=Rtn4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7, and 129SvCj7;
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT "Genomic structure and functional characterisation of the promoters of
human and mouse nogo/rtn4."
RL J. Mol. Biol. 325:299-323(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7;
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129SvCj7;
RA Van der Putten H., Mir A.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102280; AAM73502.1; -.
DR EMBL; AY102286; AAM73507.1; -.
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0001525; P:angiogenesis; IMP.
DR GO; GO:0007399; P:neurogenesis; IDA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS0845; RETICULON; 1.
SQ SEQUENCE 1046 AA; 114221 MW; 8CE2E2238ED51222 CRC64;

Query Match 55.4%; Score 1010.2; DB 2; Length 1046;
Best Local Similarity 29.2%; Pred. No. 4.3e-24;
Matches 249; Conservative 25; Mismatches 80; Indels 498; Gaps 14;

QY 5 DOSSLVSSSTDSPPPPPA-----PKYQVTPPEDE----- 35
DB 197 DKEDLVCSAALNPQESPATLTKVVKEDGWSPEKTMDFNEMKMSVAVPVREYADF KP 256
QY 36 -----EDEEEDEDEDE----- 50
DB 257 FEQANEVKDITYGSRDVLAAANMESKVDKCFEDSLQKHGKQSESNENASFPRTPE 316
QY 51 -----LEELEVLERKPAAGLSAAAVPP 72
DB 317 LVKDGSRVITCDSPSSATESTAANIFPVLEDHTSENKTDKKIEERK-AQIIETKSP 374
QY 73 AAAAPLLDFSSDS-----VPPAPRGPLPAAPPAERQ----- 105
DB 375 KTSNPFVAIHDSADYVTTNLSKVTAEVATMPEGLTDLVQACSESLNEATGTGKIA 434
QY 106 -----PSWERSPAAPAPSLP-----PAAAVLPSPKLPEDD 134
DB 435 YETKVDLVQTSIAQESYPTAQLCPSEAEATPSVLPDVMAPLNSLLPSTGASVA 494
QY 135 EP-----PARPPP----- 142
DB 495 QPSASPLEVPSPVSDGKLEPENPPVEAMSVALKTSDSKEEIKEPESFNAAQAEAA 554
QY 143 -----PPPA-----GASPLAEP-----A 156
DB 555 PYISIACDLIKTKLSTPSPFSNYSYETIAKPEKSVDPHCELVDSSPESEPVDFLSDS 614

QY 157 PPSTP-----AAPKRG----- 168
DB 615 IPEVPQTOEEAVMLMKESLITVSETVTOHKHKLRSASPQEVGKPYLESFQPNLHITKDA 674
QY 169 ----- 168
DB 675 ASNEIPTLTKKETISLQMEEFNTAIYSNDLLSSKEDKMKSETPSDSSPIEIIDEFPTF 734
QY 169 -----SG----- 170
DB 735 VSAKDDSPKEYTDLEVSNNKSEIANVQSGANSLPCSLSEPKNTYPKDEAHVSDEFSK 794
QY 171 ----- 170
DB 795 SRSSSVKVPDLLPNVSALESQIEMGNIVPKVLTKEAEKLPDSTEKEDRSITAVLSAEL 854
QY 171 --SSVVDLLYWRDIKKTGVFGASLFLLSLTVFSIVSTAYIALALLSVTISPRIYKGV 228
DB 855 NKTSVVDLLYWRDIKKTGVFGASLFLLSLTVFSIVSTAYIALALLSVTISPRIYKGV 914
QY 229 IOATOKSDEGHPPFRAYLSEVAISELVOKYSNSALGHVNSTIKELRRLFLVDDLVDSLK 288
DB 915 IOATOKSDEGHPPFRAYLSEVAISELVOKYSNSALGHVNSTIKELRRLFLVDDLVDSLK 974
QY 289 FAVLMWVFTYVYGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKI 348
DB 975 FAVLMWVFTYVYGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKI 1034
QY 349 QAKIPGLKPKAD 360
DB 1035 QAKIPGLKPKAE 1046

RESULT 12
Q80W95 PRELIMINARY; PRT; 578 AA.
AC Q80W95;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Nogo-A (Fragment).
GN Name=Nogo-A;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tozaki H., Hirata T.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073672; BAC75974.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS0845; RETICULON; 1.
FT NON TER 1
SQ SEQUENCE 578 AA; 63696 MW; 832670C171B4AC61 CRC64;

Query Match 54.4%; Score 992.2; DB 2; Length 578;
Best Local Similarity 42.4%; Pred. No. 4.1e-24;
Matches 233; Conservative 13; Mismatches 79; Indels 225; Gaps 8;

QY 17 PPRPPP---AFKYQVTPPEDEDEDEDEDEDE-----DLEELEVLERKPA 63
DB 48 PENPPPYEAMSVALKTSDAKEEIKEPESFNAAQAEAPYISACDLIKTKLSTEPSP 107
QY 64 GLS-----AAAVP-----PAAAPLLDFSSDSVPPAPR----- 91
DB 108 GFSNYSYETIAKPEKSVDPHCELVDSSPESEPVDFLSDSIPEVPTQEEAVMLMKESL 167
QY 92 -----GPLPAAPPAERQ----- 106
```

Db 168 VSETVQHKKHERLSASPOEVGKPYLESFQPNLHITKDAASNEIPTLTCKTETISLQMEEF 227
QY 107 -----
Db 228 NTAIYNSDILLSSKEDKMKESFTSDSSPIEIIIDBPPTFVSADKSPKEYTDLVSNKSE 287
QY 107 -----
Db 288 IANVSGANSPLCSSELPDCLSFKNTPKDEAHVSEFSSKRSVSKVPLPNNVSALESQ 347
QY 129 -----
Db 348 IEMGNIVKPKVLTKEAEKLPSTDEKDR-----SLTAVLSAELNK 388
QY 171 SSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVYAIALLSVTISPRIYKGVITQ 230
Db 389 TSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVYAIALLSVTISPRIYKGVITQ 448
QY 231 AIQKDEGHPPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVLSLQKA 290
Db 449 AIQKDEGHPPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVLSLQKA 508
QY 291 VLMWVFTYVGLFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOA 350
Db 509 VLMWVFTYVGLFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOA 568
QY 351 KIPGLKRXAD 360
Db 569 KIPGLKRXAE 578
RESULT 13
ID Q8K290 PRELIMINARY; PRT; 639 AA.
AC Q8K290;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-WAR-2004 (TREMELrel. 26, Last annotation update)
DE Rtn4 protein.
GN Name=Rtn4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC032192; AAH32192.1; --
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS00845; RETICULON; 1.
SQ SEQUENCE 639 AA, 70312 MW, 309A19DA37603F11 CRC64;
Query Match 54.2%; Score 988.7; DB 2; Length 639;
Best Local Similarity 42.2%; Pred. No. 6.8e-24;
Matches 232; Conservative 14; Mismatches 79; Indels 225; Gaps 8;
QY 17 PRRPP---AFKYQVTEPEDEDEDEDEDEDEDE-----DLEELVLERKPA 63
Db 109 PENPPPYEAMSVALKTSDAKEEIKPESEFNAAQAEAPYISICDLIKETKLTSTPSP 168
QY 64 GLS-----AAAVP-----PAAAPLLDFSSDSVPPAPR----- 91
Db 169 EFSNYSETAKESVPDHCFLVDDSSPESEPVDFDSDSIPVPTQBEAVMLKESLTE 228
QY 92 -----GFLPAPPAAPERQP----- 106
Db 229 VSETVQHKKHERLSASPOEVGKPYLESFQPNLHITKDAASNEIPTLTCKTETISLQMEEF 288
QY 107 ----- 106
Db 289 NTAIYNSDILLSSKEDKMKESFTSDSSPIEIIIDBPPTFVSADKSPKEYTDLVSNKSE 348
QY 107 -----SWERSPAAPAPSLPAAAVLPS- 128
Db 349 IANVSGANSPLCSSELPDCLSFKNTPKDEAHVSEFSSKRSVSKVPLPNNVSALESQ 408
QY 129 -----KLPEDEPPAPPPPPPPAGASPLAEPAPSTPAAPKRRGSG 170
Db 409 IEMGNIVKPKVLTKEAEKLPSTDEKDR-----SLTAVLSAELNK 449
QY 171 SSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVYAIALLSVTISPRIYKGVITQ 230
Db 450 TSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVYAIALLSVTISPRIYKGVITQ 509
QY 231 AIQKDEGHPPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVLSLQKA 290
Db 510 AIQKDEGHPPFRAYLESEVAISEELVQKYSNLSALGHVNSTIKELRRLFLVDDVLSLQKA 569
QY 291 VLMWVFTYVGLFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOA 350
Db 570 VLMWVFTYVGLFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDMAKIOA 629
QY 351 KIPGLKRXAD 360
Db 630 KIPGLKRXAE 639
RESULT 14
ID Q6RSS8 PRELIMINARY; PRT; 658 AA.
AC Q6RSS8;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Neurite outgrowth inhibitor NOGO-A (Fragment).
GN Name=NOGO;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX CALTHARP S.A., PIRA C.U., McNeill D.S., Liwnicz B.H., Oberg K.C.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY494005; AAS18427.1; --
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.

```
DR InterPro: IPR003388; Reticulon.
DR Pfam: PF02453; Reticulon; 1.
DR PROSITE: PS50845; RETICULON; 1.
FT NON_TER 1
SQ SEQUENCE 658 AA; 72075 MW; 14B7A000C5E8CDA5 CRC64;
Query Match 52.7%; Score 960.5; DB 2; Length 658;
Best Local Similarity 35.5%; Pred. No. 6.1e-23;
Matches 229; Conservative 41; Mismatches 70; Indels 305; Gaps 16;
QY 3 DLDQSS-----LVSSSTSPRPPPPAF----- 24
Db 32 DLVQTSVQETLKFPVQLCPSEFSEAPSPVLPDIVMEAPLSGTAAGAEASTVQLETS 91
QY 25 -----KYQFV-----TEPED--- 34
Db 92 QLGTFVTRASYENVKKEAPPLYQEAVMNPLTQAEKEEUTLKKADRESSTSPEDLET 151
QY 35 ----- 34
Db 152 PYISACDLIKETKVGESASPLTDYSTPTITEHLSDQVSEHKELAEKLSQFGCKDLF 211
QY 35 -----EDEEE-----EDEED-----DEDELE 55
Db 212 SRQVMPDFPGKESEDQTLILNGKSVENITDEQERLVDLSLAATGKPYLESFQDELDSSK 271
QY 56 VLERKPAAGLSAAVPPAAAPL-----LDPSD---SVPPAP---RGPLPAAPPAAP 102
Db 272 IYVTPQSEP-TPAKTAKAEKIPLOMEELNALAYSTDVSVAMPKPGDGSLSPSPSVSE 330
QY 103 E-----RQPSWERSPAAPAPSLP--- 120
Db 331 DDFVMLVDPKTGTEFVAEVTDRVTHKNESKDISEIRDEKEQ-----APLTLPD 382
QY 121 -----PAAVLP SKL-----PEDE 135
Db 383 LSVRNVEVKTEDDAHALKSKLOAIDREVPVSMVSLPATGTSPSTEXEIVSVGPEAFE 442
QY 136 PPARPPPPACAGPLAEAPPTPAAPKRGSGSVVDLLYWRDIKKTGVVFGASLFL 195
Db 443 KEAE-----RGAASAKEKETAVFSA---KLVSSVVDLLYWRDIKKTGVVFGASLFL 493
QY 196 LLSLTVFSVSVTAYIALALLSVTISFRIYKGVIAIQKSDGHPFRAYLESEVAISEEL 255
Db 494 LLSLTVFSVSVTAYIALALLSVTISFRIYKGVIAIQKSDGHPFRAYLESDVAVSEEL 553
QY 256 VQYNSALCHVNSTIKELRLFLVDLVDLSKFAVLMMVFTYVGFALNGLTLILLALIS 315
Db 554 IQKYSVVLGHNGTGVKELRLFLVDLVDLSKFAVLMMVFTYVGFALNGLTLILLALIS 613
QY 316 LFSIPVYERHVOQIDHYLGLANKSVKQAMAKIQAKIPLGRKAD 360
Db 614 LFSVPVYERHQAQIDHYLGLVKNVKNVQAMAKIQAKIPLGRKTE 658
RESULT 15
RTN4_MOUSE STANDARD; PRT; 199 AA.
AC Q99F72; Q9CTE3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein).
GN Name=Rtn4; Synonyms=Nogo;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3T3-L1; TISSUE=Adipocyte;
RA Coulson A.C.; Craggs P.D.; Morris N.J.;
RT "Mouse vp20/RTN4C cDNA.";
```

```
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 170-199 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kiyosawa H.,
RA Nakiido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltas L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
CC block the regeneration of the nervous central system in adults (By
CC similarity).
CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the
CC membrane of the endoplasmic reticulum through 2 putative
CC transmembrane domains (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms may be produced;
CC Name=1;
CC IsoId=Q99P72-1; Sequence=Displayed;
CC -!- SIMILARITY: Contains 1 reticulon domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF326337; AAK08076.1; -.
CC EMBL; AK003859; -. NOT ANNOTATED_CDS.
CC MGI; MGI:1915835; Rtn4.
CC GO; GO:0005783; C:endoplasmic reticulum; IDA.
CC GO; GO:0030176; C:integral to endoplasmic reticulum membrane; ISS.
CC GO; GO:0005635; C:nuclear membrane; ISS.
CC GO; GO:0005515; F:protein binding; ISS.
CC GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
CC GO; GO:0030517; P:negative regulation of axon extension; ISS.
CC GO; GO:0007399; P:neurogenesis; IDA.
CC InterPro; IPR003388; Reticulon.
CC Pfam; PF02453; Reticulon; 1.
CC PROSITE; PS50845; RETICULON; 1.
CC Alternative splicing; Endoplasmic reticulum; Transmembrane.
KW DOMAIN 1 25 Cytoplasmic (Potential).
FT TRANSMEM 26 50 Potential.
```

```
FT DOMAIN      51 137 Lumenal (Potential).
FT TRANSMEM   138 162 Potential.
FT DOMAIN     163 199 Cytoplasmic (Potential).
FT DOMAIN      12 199 Reticulon.
SQ SEQUENCE   199 AA; 22466 MW; 07BE5D580059ED9C CRC64;

Query Match      50.1%; Score 914; DB 1; Length 199;
Best Local Similarity 83.3%; Pred. No. 1.2e-22;
Matches 190; Conservative 3; Mismatches 5; Indels 30; Gaps 2;

QY 133 DDEPPARPPPPAGASPLAEPAPPPSTPAAPKRRGSGSVVDLLYWRDIKKTGVVFGAS 192
Db 2 DDQ-----KRWK-DKVVDLLYWRDIKKTGVVFGAS 31

QY 193 LFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDGHPHPRAYLESEVAIS 252
Db 32 LFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDGHPHPRAYLESEVAIS 91

QY 253 BELVOKYSNSALGHVNSTIKELRRLFLVDLDVDSLKFVLMVFTYVVGALFNGLTLLILA 312
Db 92 BELVOKYSNSALGHVNSTIKELRRLFLVDLDVDSLKFVLMVFTYVVGALFNGLTLLILA 151

QY 313 LISLFSIPVIYERHQVIDHYLGLANKSVKDMAKIQAKIPGLKRRAD 360
Db 152 LISLFSIPVIYERHQVIDHYLGLANKSVKDMAKIQAKIPGLKRRAE 199
```

Search completed: June 23, 2005, 10:55:54
Job time : 118.842 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2005, 09:47:53 ; Search time 30.5423 Seconds
(without alignments)
882.327 Million cell updates/sec

Title: US-09-830-972-29-FUSED

Perfect score: 1850

Sequence: 1 MEDLDQSLVSSSDSPRPQ.....VKDAMAKIOAKIPLKRAE 361

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.1

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*
- 2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/PTUS COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	927	50.1	199	2	US-08-700-607-1
2	927	50.1	201	4	US-09-949-016-9124
3	827.7	44.7	776	2	US-08-700-607-5
4	827.7	44.7	776	4	US-09-949-016-6998
5	804.9	43.5	439	4	US-09-949-016-9180
6	789.8	42.7	356	2	US-08-700-607-6
7	684.2	37.0	208	2	US-08-700-607-7
8	666	36.0	267	2	US-08-700-607-8
9	627.9	33.9	192	4	US-09-949-016-8859
10	599.1	32.4	588	4	US-09-949-016-7290
11	541.9	29.3	168	4	US-09-149-476-563
12	538.3	29.1	241	2	US-08-700-607-3
13	518	28.0	219	4	US-09-270-767-45132
14	348.9	18.9	75	4	US-09-621-976-4600
15	348.9	18.9	75	4	US-09-621-976-4601
16	347	18.8	68	4	US-09-513-999C-6304
17	285	15.4	92	4	US-09-149-476-411
18	276.2	14.9	1027	4	US-09-902-540-11750
19	259.7	14.0	1248	2	US-09-080-897-2
20	259.7	14.0	1248	3	US-09-323-735-2
21	258.2	14.0	1315	3	US-08-899-595-3
22	256.5	13.9	1255	2	US-09-080-897-4
23	256.5	13.9	1255	3	US-08-899-595-1
24	256.5	13.9	1255	3	US-09-323-735-4
25	248.2	13.4	114	4	US-09-513-999C-7861
26	247	13.4	2090	4	US-09-538-092-1081
27	247	13.4	2120	4	US-09-949-016-9768

28	246.1	13.3	8991	4	US-08-714-741-32	Sequence 32, Appl
29	245.8	13.3	1070	3	US-08-922-635-22	Sequence 22, Appl
30	245.8	13.3	1504	4	US-09-364-206-2	Sequence 2, Appl
31	244.5	13.2	990	4	US-09-949-016-10562	Sequence 10562, A
32	243.6	13.2	1719	2	US-08-459-568-4	Sequence 4, Appl
33	243.6	13.2	1719	2	US-08-399-411-4	Sequence 4, Appl
34	243.6	13.2	1719	3	US-08-516-859A-4	Sequence 4, Appl
35	243.6	13.2	1719	3	US-09-586-472-4	Sequence 4, Appl
36	243.6	13.2	1719	4	US-09-528-706-4	Sequence 4, Appl
37	241.5	13.1	933	3	US-08-764-870-14	Sequence 14, Appl
38	241.5	13.1	933	3	US-08-980-115-14	Sequence 14, Appl
39	238.7	12.9	1540	4	US-09-949-016-11382	Sequence 11382, A
40	238.7	12.9	1540	4	US-09-949-016-11383	Sequence 11383, A
41	238.7	12.9	1706	2	US-08-459-568-2	Sequence 2, Appl
42	238.7	12.9	1706	2	US-08-399-411-2	Sequence 2, Appl
43	238.7	12.9	1706	3	US-08-516-859A-2	Sequence 2, Appl
44	238.7	12.9	1706	3	US-09-586-472-2	Sequence 2, Appl
45	238.7	12.9	1706	4	US-09-528-706-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-700-607-1
; Sequence 1, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hallman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Consensus
; US-08-700-607-1

Query Match 50.1%; Score 927; DB 2; Length 199;
Best Local Similarity 100.0%; Pred. No. 1.1e-33;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 174 VVDLLYWRDIKKTGVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 233

Db 12 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 71
QY 234 QKSDGHPHPRAYLESEVAISEELVOKYNSALGHVNCITIKELRRLFLVDDLVDLSLKPAVL 293
Db 72 QKSDGHPHPRAYLESEVAISEELVOKYNSALGHVNCITIKELRRLFLVDDLVDLSLKPAVL 131
QY 294 MVVFTYVGFALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKI 353
Db 132 MVVFTYVGFALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKI 191
QY 354 PGLKRAE 361
Db 192 PGLKRAE 199
RESULT 2
US-09-949-016-9124
; Sequence 9124, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9124
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9124
Query Match 50.1%; Score 927; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.1e-33;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 174 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 233
Db 14 VVDLLYWRDIKKTGVVFGASFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 73
QY 234 QKSDGHPHPRAYLESEVAISEELVOKYNSALGHVNCITIKELRRLFLVDDLVDLSLKPAVL 293
Db 74 QKSDGHPHPRAYLESEVAISEELVOKYNSALGHVNCITIKELRRLFLVDDLVDLSLKPAVL 133
QY 294 MVVFTYVGFALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKI 353
Db 134 MVVFTYVGFALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKI 193
QY 354 PGLKRAE 361
Db 194 PGLKRAE 201
RESULT 3
US-08-700-607-5
; Sequence 5, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Forter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 776 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307307
US-08-700-607-5
Query Match 44.7%; Score 827.7; DB 2; Length 776;
Best Local Similarity 27.1%; Pred. No. 3.6e-28;
Matches 196; Conservative 55; Mismatches 89; Indels 383; Gaps 17;
QY 6 QSP----- 9
Db 70 QSPVAMETASTAGVAGVSSAMDHFTSTSKDGEBCYTSLSIDICYPPQEDSTYFTGLOK 129
QY 10 ----VSSSDSPR---POP----- 21
Db 130 ENGHVTISEFEELTGPSPIDVPGIESRGLFSSDSGIEMTPAESTEVNKILADPLDQM 189
QY 22 ---AFKYQVREPEDEEEEEDEDEDELE----- 50
Db 190 KAEVKYIDITRPEVBKQEQHPELDKLDKFKNDTDSIKPGVREPKPAPVEGKI 249
QY 51 -----ELE----- 53
Db 250 IKDHLLBESTFAPYIDDLSEBORRAPQITTPVKITLITIEPVSVEVTTQKTEKODICUK 309
QY 54 -----VLERKPAAGLS-- 64
Db 310 PSPDPTVTVTSEPEDDSPGSIPTPSSGTEPSAESQKGSISEDELITAIKEAGLSYE 369
QY 65 ----AAPV-----PTAPAGAPL----- 78
Db 370 TAENPRPVQLADRPVKARSGPPTIP---SPLDHEASSAESGDSIEILVSDPMAEDA 426
QY 79 -----MDGNDVFPAPRGPPLPAPPV-----APE 103
Db 427 LPSGYVSFGHVGPP-----PSPASPSIQYSILREREAELOSELIESCDASASESPK 482
QY 104 RO---PSWDPPSVS-----STVPAPSLPAAAAVP 130
Db 483 REQDSPPMKPSALDAIRETGVAERAPSRRLAEPGSLDYPSTEPQGP----- 534
QY 131 SKLPEDD-----EPPARPPPPPPASVQAEVWTPAP-APAAP-----STSVDDL 178
Db 535 -ELPPGDGALEPETMPLPRKPEEDSSNQSPAATKPGPLGPGAPPLFLNKKAKIDL 593

Db 247 LNKQKAIIDLYWRDIKQGIYVGFSGFLLLSLFTQSVSVVAYLALALASATISFRIYKS 306
 QY 229 VIOAIQKSDGHPFRAYLSEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDLSL 288
 Db 307 VLQAVQKTDGHPFRAYLSEITLSQEQIKYKTDCLQFYVNSTKLRLFLVQDLVDLSL 366
 QY 289 KEAVLMWVTYVYCALFNGLTLLILALISLFSVPVIYERHQAQIDHYGLGANKVNDAMAK 348
 Db 367 KEAVLMWLTYYGALFNGLTLLMAVSMFTLPVVYVYHQAQIDQYLGVLVRTHINAVAK 426
 QY 349 IQAKIPGLKRAE 361
 Db 427 IQAKIPGAKRAE 439

RESULT 6
 US-08-700-607-6
 ; Sequence 6, Application US/08700607
 ; Patent No. 5858708
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Au-Young, Janice
 ; APPLICANT: Goli, Surya K.
 ; APPLICANT: Hillman, Jennifer L.
 ; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: U.S.
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/700,607
 ; FILING DATE: Filed Herewith
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0114 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 356 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 307309
 ; US-08-700-607-6

Query Match 42.7%; Score 789.8; DB 2; Length 356;
 Best Local Similarity 42.6%; Pred. No. 3.9e-27;
 Matches 169; Conservative 42; Mismatches 74; Indels 112; Gaps 10;
 QY 16 PPRP-QPAFKYQVREPEDEE-----EEEEEEEEDEDELEEVLERK 58
 Db 21 PPSPASPSIQXSLRREARELDSLIIESCDASSASESPKREQD----- 66
 QY 59 PAAGLSAAVPTAPAGALPMDFGNDVPPAPRGPLPAAPPVAP-----E 103
 Db 67 -----SPPMKPSALDAIREETGVRAEE 88

QY 104 ROPS-----WDPG---PVSVTPAPSPLSAAVSPSKLPEDD-----EPPARPPPPPPASV 151
 Db 89 RAPSRRLAEPGSGFDYFSTPEPQGP-----ELPPGGLALPEPETPMLPRKPEEDSS 139
 QY 152 SPQAEFVWTPAP-APAAAPP-----STSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFS 204
 Db 140 SNQSPAATKPGPLGPGAPPLFLNKAIDLLYWRDIKQTGIVFGSFLLLLSLTQFS 199
 QY 205 IVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLSEVAISELVQKYSNSA 264
 Db 200 VVSVVAYLALALASATISFRIYKSVLQAVQKTDGHPFKAYLEITLSQEQIKYKTDCL 259
 QY 265 LGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVTYVYVGLFNGLTLLILALISLFSVPVIY 324
 Db 260 QFYVNSTKLRLFLVQDLVDLSLKFVLMWLTYYGALFNGLTLLMAVSMFTLPVVY 319
 QY 325 ERHQAQIDHYGLGANKVNDAMAKIQAKIPGLKRAE 361
 Db 320 VKHQAQIDQYLGVLVRTHINAVVAKIQAKIPGAKRAE 356

RESULT 7
 US-08-700-607-7
 ; Sequence 7, Application US/08700607
 ; Patent No. 5858708
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Au-Young, Janice
 ; APPLICANT: Goli, Surya K.
 ; APPLICANT: Hillman, Jennifer L.
 ; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: U.S.
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/700,607
 ; FILING DATE: Filed Herewith
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0114 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 208 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 307311
 ; US-08-700-607-7

Query Match 37.0%; Score 684.2; DB 2; Length 208;
 Best Local Similarity 62.4%; Pred. No. 6.7e-23;
 Matches 131; Conservative 35; Mismatches 36; Indels 8; Gaps 1;
 QY 152 SPQAEFVWTPAPAPAPPESTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSVTAY 211
 Db 7 STKMDCVW-----SNWKSQAIDLLYWRDIKQTGIVFGSFLLLLSLTQFSVSVVAY 58

Qy	212	I A L A L L S V T I S F R I Y K V G V I O A I Q K S D E G H P P R A Y L E S E V A I S E E L V O K T S N S A L G H V N C T	271
Db	59	L A L A A L S A T I S F R I Y K S V L O A V Q K T D E G H P P R A Y L E S I T L S Q E Q I Q K Y T D C L Q F V N S T	118
Qy	272	I K E L R R L F L V D D L V D S L A F A V L M W V T V Y G A L F N G L T L L I L A I S I P S V P V I Y E R H Q A I	331
Db	119	L K E L R R L F L V Q D L V D S L A F A V L M W L L T V Y G A L F N G L T L L M A V S M F L P V V Y V K H Q A I	178
Qy	332	D H Y I G L A N K N V K D A M A K I O A K I P G U R K A E	361
Db	179	D O Y L G L V R T H I N A V V A K I O A K I P G A K R H A E	208

```

RESULT 8
US-08-700-607-8
; Sequence 8, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennif L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 281046
US-08-700-607-8

```

Db 130 VLMWLLTVVGVGALFNGLTLLMAVVSMTFLPVVVYVYKHQAQVDQYLGIVRTHINTVTVAKIOA 189

Qy 352 KIPGLK 357
|||||:

Db 190 KIPGAR 195

RESULT 9

US-09-949-016-8859

; Sequence 8859, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 8859

; LENGTH: 192

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-8859

Query Match 33.9%; Score 627.9; DB 4; Length 192;

Best Local Similarity 61.1%; Pred. No. 1.8e-20;

Matches 116; Conservative 38; Mismatches 35; Indels 1; Gaps 1;

Qy 173 SVDDLWVRDIKTKGVVFGASLFLLLSLTVFVSIVSVTAYIALALLSVTISFRIYKGVIOA 232

Db 3 SVHDLIFWRDVKTKGFVFGTTLMLLSLAAPSVISVSYLTALLSVTISFRIYKSVIOA 62

Qy 233 IQSDDEGHPRAYLSEVAISEELVQKYSNSALGHVNCITKELRRLFLVDDLVDSLKEAV 292

Db 63 VQKSEEGHPKAYLDVDDITTSSEAFHNYMNAAMVHINRALKLIIRLFLVEDLVDSLKLAV 122

Qy 293 LMMVFTVVGALFNGLTLLALISLFSVPVPIYERHQAQIDHYLGLANKNVKDAMAKIOAK 352

Db 123 FMWLMTVGVAFNGITLILIAELLIFSVPVPIYEEKYKQIDHYVGIARDQTKSIVEKIOAK 182

Qy 353 IPGL-KKAE 361

Db 183 LPGIKKAE 192

RESULT 10

US-09-949-016-7290

; Sequence 7290, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7290

```
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7290

Query Match          32.4%; Score 599.1; DB 4; Length 588;
Best Local Similarity 26.9%; Pred. No. 2.8e-18;
Matches 157; Conservative 56; Mismatches 122; Indels 249; Gaps 18;

QY 14 DSDPRPQ-----PAFKYQFVRE-----PEDEE----- 35
Db 18 DERPRPRAAGGTAGVGGPDAGRGAMGVLPFAH--CKEAPSTASSTPDTSTEGNDSDS 75
QY 36 -----EEEEEEED----- 46
Db 76 DPRELHTAREFSEDEEEETTTT----- 135
QY 47 -----EDLELEVLERKPAAGLSAAPVPTAPAGAPLMD--FGNDFFVPPAP 90
Db 136 VSEPRDOHPQPSLGLSDLESIPLSQSPFERRGDP-DTAPPSPERPLEDLRLDLHLGWVA 194
QY 91 RG-----PLPAAPPVAPER-----QPSWDP-----SPV 113
Db 195 RGTGSGEDSSSTSTPLEDEEPEQPNRLTGEAGEELDLRLRLAOPS-SPEVLTPQLSPG 253
QY 114 SSTVPAPSLAANVSPSKLPEDDEPPAP----- 143
Db 254 SGTPOAGTP-----SPSRSDNSNGPEEPLEEEBKONGPLEREPVRGQCCLDSTDQLF 307
QY 144 -----PPPPASVSPQAEPVW-----TPP----- 162
Db 308 TVEPRLLGTAMWLKTSLLAVKVPILLESP---PLMTATGWQVGRPTPTPVLRULL 364
QY 163 -----APAPAAPSTST-----VDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVA 210
Db 365 KWAKSPRSSGVPSSLGADMGSKVADLLYWKDTRTSGVVFTGLMWSLCLLHFSIVSVA 424
QY 211 YIALALLSVTIFRIYKGVIOAKQSDGHPRAVLESEVAISEELVQKYSNLSALGVNC 270
Db 425 HLALLLCCTISLRVYKRVQLAVHRGDGANPFQAYLDVDTITRQTERLSHQITSRVVS 484
QY 271 TIKELRRLFLVDLSDLSKFVLMVFTVVGALFNGLLTLLIALISLFSVPVYERHQ 330
Db 485 AATQLRHFLVEDVDSLKLALLFYLTFTVGAIFNGLLTLLILGVGLFTPIPLLYRQHQ 544
QY 331 IDHYGLANKNVKDMAKTQAKIPGL-----KKRAE 361
Db 545 IDQYVGLVTLNQLSHIKAKIRAKIPGTGALASAAAAVSGSKAKAE 588

RESULT 11
US-09-149-476-563
; Sequence 563, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002PI
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
```

EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,889
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,893
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,630
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,878
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,662
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,872
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,882
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,637
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,903
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,888
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,879
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,880
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,894
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,911
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,636
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,874
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,910
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,864
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,631
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,845
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,599
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,585
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,589
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501

EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 29.3%; Score 541.9; DB 4; Length 168;
Best Local Similarity 60.5%; Pred. No. 8.9e-17;
Matches 101; Conservative 34; Mismatches 31; Indels 1; Gaps 1;

QY 196 LLSLTVESIVSVTAIYIALLSVTISPRIYKGVIOAQKSDGHPFRAYLESEVAISSE 255
Db 1 MLLSLAASFVSISVSVISLILLSVTISPRIYKSVIOAQKSEGHFFKAYLDVDTLSSE 60
QY 256 LVQKYSNSALGHVNCTIKELRRLFLVDLVDLSKFAVLMMVFTYYGALFNGLTLTLALI 315
Db 61 AFHNTYMAVHINERALKLIIRLFVEDLVDLSKLAFLVFWLMTYYGAVENGITLLILAEI 120
QY 316 SLFSPVPIYERHQAIIDHYGLANKVNDMAKIOAKIPGL-KRKAE 361
Db 121 LIFSVPVIVYKQIDHYGVGIARDQTKSIVEKIOAKLPGIARKKAE 167

RESULT 12
US-08-700-607-3
Sequence 3, Application US/08700607
Patent No. 5858708
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

This Page Blank (uspto)


```
QY 172 ----- 171
Db 421 DKCFADSLQTNHKESSNDTSFPSTPEGIKDRSGAYITCAPFNPAAATESIATNIF 480
QY 172 ----- 171
Db 481 PLLGDPSTSENKTKDEKKIEBKKAQIVTEKNTSTKTSNPFVAAQDSETDVTTDNLTKYTE 540
QY 172 ----- 171
Db 541 EVVANMPEGLTDLVQEAACESLNEVTGKIAYETKMDLVQTSVMQESLYPAAQLCPSE 600
QY 172 ----- 171
Db 601 ESEATPSVPLDVIWEAPLNSAVFSAGASVIQSPSSPLEASSVNYESIKHEPENPPYE 660
QY 172 ----- 171
Db 661 EAMSVLKKVSGIKKEIKEPENINAAQTEAPYISACDLIKETKLSAEPAPDFSDYSE 720
QY 172 ----- 171
Db 721 MAKVEQVPDHSSELVEDSSPDSEPVDFSDDSIPDVQKQDETVMVKESLTETSFESMI 780
QY 172 ----- 171
Db 781 EYENKEKLSALPPBGGKPYLESFKLSLNTKDTLLPDEVSTLSKKEKIPLOMEELSTAVY 840
QY 172 ----- 171
Db 841 SNDDLFIKSEAQIRETETFSDSPIEIDEFFTLISSKTDSPSKLAREYTDLEVSHKSEI 900
QY 172 ----- 171
Db 901 ANAPDAGSLPCTELPHDLNLKNIQPKVEKISFSDPSKNGSATSKVLLLPDVVSALAT 960
QY 172 ----- 171
Db 961 QAEIESIVKPKVLVKEAEKLPDTEKEDRSFSAELSSTSVVLDLYMRDIKKTGVV 1020
QY 190 FGASFLLLSLTVFSIVSVTAIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLSE 249
Db 1021 FGASFLLLSLTVFSIVSVTAIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLSE 1080
QY 250 VAISELVQKYSNLSALGHVNCITKELRRLFLVDDLVDLSLKFAVLMMVFTYVGALFNGTL 309
Db 1081 VAISELVQKYSNLSALGHVNCITKELRRLFLVDDLVDLSLKFAVLMMVFTYVGALFNGTL 1140
QY 310 LILALISLFSVPVIVYERHQAQIDHYGLGANKNVKDMAKIOAKIPGLKRAE 361
Db 1141 LILALISLFSVPVIVYERHQAQIDHYGLGANKNVKDMAKIOAKIPGLKRAE 1192

RESULT 11
US-09-893-348-23
; Sequence 23, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: COHEN, Irun R.
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; FILE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
```

```
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-348-23
```

```
Query Match 95.0%; Score 1756.9; DB 9; Length 1192;
Best Local Similarity 30.3%; Pred. No. 3.2e-52;
Matches 361; Conservative 0; Mismatches 0; Indels 831; Gaps 1;

QY 1 MEDLQSQSLVSSSDSPRPQPAFKYQFVREPEDEEEDEDEDEDELEELVLERKPA 60
Db 1 MEDLQSQSLVSSSDSPRPQPAFKYQFVREPEDEEEDEDEDEDELEELVLERKPA 60
QY 61 AGLSAAPVPTAPAGAPLMDFGNDVFPAPRGPLPAAPVAPERQPSWDPPSVSTVPAP 120
Db 61 AGLSAAPVPTAPAGAPLMDFGNDVFPAPRGPLPAAPVAPERQPSWDPPSVSTVPAP 120
QY 121 SPLSAAVSPSKLPEDDEPPARPPPPASVSPQAEVMTTPPAPAPAAPPS----- 171
Db 121 SPLSAAVSPSKLPEDDEPPARPPPPASVSPQAEVMTTPPAPAPAAPPS----- 171
QY 172 ----- 171
Db 172 ----- 171
QY 181 SSGSVDETFLFALPAASEPVISSAENMDLKEQPGNTISAGQEDFPFVLETAASLPISLP 240
Db 172 ----- 171
QY 241 LSAASFKEHYGLNLSVLPTTEGLQENVSEASKEVSEKAKTLIDRLDTFSELEYSEM 300
Db 172 ----- 171
QY 301 GSSFSVSPKAESAVIVANPREIIVKNDKEEKLVSNNILHNQQLPTALTAKLVEDEVV 360
Db 172 ----- 171
QY 361 SSEKAKDSFNEKRVAVEAPMBEEVADFKPFRVMEVKDSKEDSDMLAAGKIESNLSKV 420
Db 172 ----- 171
QY 421 DKCFADSLQTNHKESSNDTSFPSTPEGIKDRPGAYITCAPFNPAAATESIATNIF 480
Db 172 ----- 171
QY 481 PLLGDPSTSENKTKDEKKIEBKKAQIVTEKNTSTKTSNPFVAAQDSETDVTTDNLTKYTE 540
Db 172 ----- 171
QY 541 EVVANMPEGLTDLVQEAACESLNEVTGKIAYETKMDLVQTSVMQESLYPAAQLCPSE 600
Db 172 ----- 171
QY 601 ESEATPSVPLDVIWEAPLNSAVFSAGASVIQSPSSPLEASSVNYESIKHEPENPPYE 660
Db 172 ----- 171
QY 661 EAMSVLKKVSGIKKEIKEPENINAAQTEAPYISACDLIKETKLSAEPAPDFSDYSE 720
Db 172 ----- 171
QY 721 MAKVEQVPDHSSELVEDSSPDSEPVDFSDDSIPDVQKQDETVMVKESLTETSFESMI 780
Db 172 ----- 171
QY 781 EYENKEKLSALPPBGGKPYLESFKLSLNTKDTLLPDEVSTLSKKEKIPLOMEELSTAVY 840
Db 172 ----- 171
```


Db	841	SNDOLFISKEAQI	RETETFDSSPIE	IIDEPPTLIS	SKTDSF	SKLAREY	TDLEVSHKSEI	900		
Qy	172	-----	-----	-----	-----	-----	-----	171		
Db	901	ANAPDAGAGSLP	CTELPHDLSL	KNIQPVEEKI	SPSDDFS	KNGSATS	KVLLLPDVSALAT	960		
Qy	172	-----	-----	-----	-----	-----	-----	189		
Db	961	QAEIESIVK	PKVLVEAKEL	PSDTEKED	RSPSAI	PSAELSKTS	VVDLLTWDRDKKTGVV	1020		
Qy	190	FGASLFL	LLLSLTVFS	IVSVTAYI	ALALLSVT	ISPRIYK	GVIOAIQKSD	EGHPFRAYLESE	249	
Db	1021	FGASLFL	LLLSLTVFS	IVSVTAYI	ALALLSVT	ISPRIYK	GVIOAIQKSD	EGHPFRAYLESE	1080	
Qy	250	VAISEELV	QKYSNSAL	GHNCTIK	ELRRLFL	VDDLDV	SLKFAVL	MMVFTYV	GALFNGLTL	309
Db	1081	VAISEELV	QKYSNSAL	GHNCTIK	ELRRLFL	VDDLDV	SLKFAVL	MMVFTYV	GALFNGLTL	1140
Qy	310	LILALISL	FSVPVPIY	ERHQAI	DHYLGL	ANQNVK	DAMAKI	OAKIPGL	KRAE	361
Db	1141	LILALISL	FSVPVPIY	ERHQAI	DHYLGL	ANQNVK	DAMAKI	OAKIPGL	KRAE	1192

RESULT 12

```

US-09-972-599A-6
; Sequence 6, Application US/09972599A
; Patent No. US20020077295A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
; FILE REFERENCE: C077 CIP US
; CURRENT APPLICATION NUMBER: US/09/972,599A
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/236,378
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-599A-6

```

Query Match	95.0%	Score	1756.9	DB	9	Length	1192
Best Local Similarity	30.3%	Pred. No.	3.2e-52				
Matches	361	Conservative	0	Mismatches	0	Indels	831
Gaps	1						
Qy	1	MEDLDQSPLYSSSDSPRPQOPAFKYQVPRPEDEEEEEEDEDEDEDELEELVLRKPA	60				
Db	1	MEDLDQSPLYSSSDSPRPQOPAFKYQVPRPEDEEEEEEDEDEDEDELEELVLRKPA	60				
Qy	61	AGLSAAPVPTAPAAAGAPLMDFGNDVFPAPRGPLPAAPVPA PRQPSWDSPSVSSTVPAP	120				
Db	61	AGLSAAPVPTAPAAAGAPLMDFGNDVFPAPRGPLPAAPVPA PRQPSWDSPSVSSTVPAP	120				
Qy	121	SPLSAAAVSPSKULPEDDEPPARPPPPPPASVQAEFVWTPPPAPAAPPS	171				
Db	121	SPLSAAAVSPSKULPEDDEPPARPPPPPPASVQAEFVWTPPPAPAAPPS	180				
Qy	172	-----	171				
Db	181	SSGSVDETLFPALPAASEFVIRSSAENMDLKEQPGNTISAGQEDFPVSVLLETAASLP	240				
Qy	172	-----	171				

RESULT 13

RES001 13
US-10-060-036-71
Sequence 71, Application US/10060036
Publication No. US20030073144A1
GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
APPLICANT: Kalos, Michael J.
APPLICANT: Lodes, Michael D.
APPLICANT: Persing, David H.
APPLICANT: Hepler, William T.


```

QY 172 ----- 171
Db 361 SSEKAKDSFNEKRVAVEAPMREYADFKPFRVWEVKDSKEDSMLAAGKIESNLESKV 420
QY 172 ----- 171
Db 421 DKCFADSLQTNHEKDSSENDTSFPSTPEGIKDRPGAYITCAPFNPAAATESIATNIF 480
QY 172 ----- 171
Db 481 PLLGDPSTENKTDKKEIEKKAQIVTEKNTSTKTSNPFVLAQDSETDVYTTDNLTKVTE 540
QY 172 ----- 171
Db 541 EVVANMPEGLTPDLVQEAACESELNEVTGTKIAYETKMDLVQTSVMQESLYPAAQLCPSP 600
QY 172 ----- 171
Db 601 ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSEPLEASSVNYESIKHEPENPPYE 660
QY 172 ----- 171
Db 661 EAMSVLKKVSGIKKEIKPENINAAQTEAPYISACDLIKETKLSAEPAPDFSDYSE 720
QY 172 ----- 171
Db 721 MAKVEQVPDHSSELVEDSPDSEPDVDFSDSIPDPVQKQDETVMVLKESLTETSFSMI 780
QY 172 ----- 171
Db 781 EYENKEKLSALPPEGKPYLESFKLSLNDTKOTLLPDEVSTLSKKEKIPLOMEELSTAVY 840
QY 172 ----- 171
Db 841 SNDDLFIKSEAQIRETETFSDDSPIEIDEFPPLISSKTDSFKLAREYTDLEVSHKSEI 900
QY 172 ----- 171
Db 901 ANAPDAGSLPCTELPHDLNLKNIQKVEKISFSDDFSKNGSATSKVLLLPDVSALAT 960
QY 172 ----- 171
Db 961 QAEIESIVKPLVKEAKKLPSTDEKDRSPSAIFSALSSTSVVDLLYWRDIKKTGVV 1020
QY 190 FGASLFLLSLTVFSIVSTAYTALALLSVTISFRYKGVIOAIQKSDGHPFRAYLESE 249
Db 1021 FGASLFLLSLTVFSIVSTAYTALALLSVTISFRYKGVIOAIQKSDGHPFRAYLESE 1080
QY 250 VAISELVQKYSNLSALGHVNCITIKELRLFLVDDLVDSLKFVLMVFTYVGLFNGLTL 309
Db 1081 VAISELVQKYSNLSALGHVNCITIKELRLFLVDDLVDSLKFVLMVFTYVGLFNGLTL 1140
QY 310 LILALISLSPVPIYERHQAQIDHYGLGNKVNKDMAKIOAKIPGLKRAE 361
Db 1141 LILALISLSPVPIYERHQAQIDHYGLGNKVNKDMAKIOAKIPGLKRAE 1192

```

```

RESULT 15
US-10-327-213-9
; Sequence 9, Application US/10327213
; Publication No. US20040121341A1
; GENERAL INFORMATION:
; APPLICANT: FILBIN, MARIE T.
; APPLICANT: DOMENICONI, MARCO
; APPLICANT: CAO, ZIXUAN
; TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (NAG)
; TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION
; FILE REFERENCE: CUNY/003
; CURRENT APPLICATION NUMBER: US/10/327,213
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9

```

```

; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-327-213-9

Query Match      95.0%; Score 1756.9; DB 16; Length 1192;
Best Local Similarity 30.3%; Pred. No. 3.2e-52;
Matches 361; Conservative 0; Mismatches 0; Indels 831; Gaps 1;

QY 1 MEDLDOSPLVSSSDSPRPQPAFKYQVREPEDEDEDEDEDEDEDEDEDEDEDELEELVKPKA 60
Db 1 MEDLDOSPLVSSSDSPRPQPAFKYQVREPEDEDEDEDEDEDEDEDEDEDEDELEELVKPKA 60
QY 61 AGLSAAPVPTAAGAPLMDFGNDFVPAPRGPPLPAAPVAPRQPSWDPSPVSVSTVPAP 120
Db 61 AGLSAAPVPTAAGAPLMDFGNDFVPAPRGPPLPAAPVAPRQPSWDPSPVSVSTVPAP 120
QY 121 SPLSAAAASPSKLPEDDEPPAPPPPPASVSQAEVPMVTPPAPAPAAPPS----- 171
Db 121 SPLSAAAASPSKLPEDDEPPAPPPPPASVSQAEVPMVTPPAPAPAAPPS----- 171
QY 172 ----- 171
Db 172 ----- 171
QY 181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPFVSLLETAASLSLP 240
Db 181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPFVSLLETAASLSLP 240
QY 172 ----- 171
Db 241 LSAAFPKEHEYLGNLSTVLPTSGTLQENVSEASKEVSEKAKTLLIDRDLTSESELEYSEM 300
QY 172 ----- 171
Db 301 GSSFSVSKAESAVIVANPREIIIVKNKDEEEKLVSNLILHNQQLPTALTTLKVEDEVV 360
QY 172 ----- 171
Db 361 SSEKAKDSFNEKRVAVEAPMREYADFKPFRVWEVKDSKEDSMLAAGKIESNLESKV 420
QY 172 ----- 171
Db 421 DKCFADSLQTNHEKDSSENDTSFPSTPEGIKDRPGAYITCAPFNPAAATESIATNIF 480
QY 172 ----- 171
Db 481 PLLGDPSTENKTDKKEIEKKAQIVTEKNTSTKTSNPFVLAQDSETDVYTTDNLTKVTE 540
QY 172 ----- 171
Db 541 EVVANMPEGLTPDLVQEAACESELNEVTGTKIAYETKMDLVQTSVMQESLYPAAQLCPSP 600
QY 172 ----- 171
Db 601 ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSEPLEASSVNYESIKHEPENPPYE 660
QY 172 ----- 171
Db 661 EAMSVLKKVSGIKKEIKPENINAAQTEAPYISACDLIKETKLSAEPAPDFSDYSE 720
QY 172 ----- 171
Db 721 MAKVEQVPDHSSELVEDSPDSEPDVDFSDSIPDPVQKQDETVMVLKESLTETSFSMI 780
QY 172 ----- 171
Db 781 EYENKEKLSALPPEGKPYLESFKLSLNDTKOTLLPDEVSTLSKKEKIPLOMEELSTAVY 840
QY 172 ----- 171
Db 841 SNDDLFIKSEAQIRETETFSDDSPIEIDEFPPLISSKTDSFKLAREYTDLEVSHKSEI 900
QY 172 ----- 171
Db 901 ANAPDAGSLPCTELPHDLNLKNIQKVEKISFSDDFSKNGSATSKVLLLPDVSALAT 960

```

```
Qy 172 -----TSVVDLLYWRDIKKTGVV 189
Db 961 QAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV 1020
Qy 190 FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESE 249
Db 1021 FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESE 1080
Qy 250 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFVLMWVFTYVGALFNGLT 309
Db 1081 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFVLMWVFTYVGALFNGLT 1140
Qy 310 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKKAE 361
Db 1141 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKKAE 1192
```

Search completed: June 23, 2005, 10:34:33
Job time : 114.151 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2005, 10:16:50 ; Search time 114.158 Seconds
(without alignments)
1223.045 Million cell updates/sec

Title: US-09-830-972-29-FUSED
Perfect score: 1850
Sequence: 1 MEDLDQSLVSSSDPPRPQ.....VKDAMAKIQKIPGLKRAE 361

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.1

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	1833.8	99.1	373	3	AAY53624 A bone ma
2	1833.8	99.1	373	3	AAY56969 Human MAG
3	1833.8	99.1	373	3	AAB24242 Human Nog
4	1833.8	99.1	373	4	AAB82350 Human NOG
5	1833.8	99.1	373	5	AAM47954 Human RTN
6	1833.8	99.1	373	5	ABP68601 Human pan
7	1833.8	99.1	373	5	ABH81079 Human neu
8	1833.8	99.1	373	7	AD163044 Human apo
9	1833.8	99.1	373	7	ADK67503 Human RTN
10	1833.8	99.1	373	8	ADP67235 Human NOG
11	1825.8	98.7	373	5	ABG30937 Human NOG
12	1756.9	95.0	1192	3	AAY56967 Human MAG
13	1756.9	95.0	1192	4	AAB82349 Human NOG
14	1756.9	95.0	1192	4	AAB82349 Human NOG
15	1756.9	95.0	1192	5	AAB82349 Human NOG
16	1756.9	95.0	1192	5	ABP68600 Human pan
17	1756.9	95.0	1192	5	ABH81078 Human neu
18	1756.9	95.0	1192	6	ABR59667 Human NOG
19	1756.9	95.0	1192	8	AD008103 Human pol
20	1756.9	95.0	1192	8	ADP45551 Human NOG
21	1756.9	95.0	1192	8	ADP67234 Human NOG
22	1756.9	95.0	1192	8	ADP67234 Human NOG
23	1749.9	94.6	1192	7	ADK67502 Human RTN
24	1749.9	94.6	1192	8	AD026400 Human tru
25	1749.3	94.6	1178	3	AAY71311 Human neu

26	1556.2	84.1	379	7	ADB85283	Adb85283 Rat fooc
27	1551.6	83.9	361	3	AAY71385	Aay71385 Alternati
28	1549.3	83.7	359	3	AAY71558	Aay71558 Rat Nogo
29	1546.3	83.6	360	3	AAY71383	Aay71383 Rat neuro
30	1546.3	83.6	360	5	ABB81076	Abb81076 Rat neuro
31	1480.5	80.0	360	4	AAE03987	Aae03987 Human gen
32	1478.8	79.9	1163	3	AAY71310	Aay71310 Rat neuro
33	1478.8	79.9	1163	3	AAY71384	Aay71384 Alternati
34	1478.8	79.9	1163	5	ABB81074	Abb81074 Rat neuro
35	1478.8	79.9	1163	8	ADO26399	Ado26399 Rat trunc
36	1478.8	79.9	1163	8	ADP45572	Adp45572 Rat NogoA
37	1476.8	79.8	1162	3	AAY71557	Aay71557 Rat Nogo
38	1475.2	79.7	1246	4	AAU33228	Aau33228 Novel hum
39	1455.3	78.7	1162	8	ADP89537	Adt89537 Mus muscu
40	1441.2	77.9	1163	8	ADO08105	Ado08105 Mouse pol
41	1324.8	71.6	291	4	AAM93484	Aam93484 Human pol
42	1324.8	71.6	291	8	ADL31138	Adl31138 Human pro
43	1234.5	66.7	973	8	ADQ16420	Adq16420 Fusion pr
44	1028	55.6	893	3	AA95012	Aay95012 Human sec
45	1028	55.6	983	6	ABU11573	Abu11573 Human MDD

ALIGNMENTS

RESULT 1
AAY53624
ID AAY53624 standard; protein; 373 AA.

AC AAY53624;

DT 22-FEB-2000 (first entry)

DE A bone marrow secreted protein designated BMS112.

KW Bone marrow secreted protein; bone marrow stromal cell; cytokine;
KW cell proliferation; cell differentiation; hematopoiesis; anaemia;
KW myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;
KW erythroid progenitor cell; colony stimulating factor; granulocyte;
KW monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;
KW platelet disorder; thrombocytopenia; hematopoietic stem cell;
KW stem cell disorder; aplastic anaemia; bone differentiation;
KW paroxysmal nocturnal hemoglobinuria; bone growth; cartilage;
KW ligament; nerve; wound healing; tissue repair; burn; incision; ulcer;
KW bone fracture; cartilage damage; artificial joint.

OS Homo sapiens.

PN WO9933979-A2.

PD 08-JUL-1999.

PF 18-DEC-1998; 98WO-US027008.

PR 30-DEC-1997; 97US-0068958P.

PR 24-SEP-1998; 98US-0101603P.

PR 30-SEP-1998; 98US-0102540P.

PA (CHIR) CHIRON CORP.

PI Lin H, Cao L;

DR WPI; 2000-038344/03.

XX N-PSDB; AAZ36230.

PT New isolated human polynucleotide and secreted proteins can induce

PT production of other cytokines in certain cell populations.

PS Claim 2; Page 74; 120pp; English.

CC AAY53622-43 represent bone marrow secreted proteins of human bone marrow
CC stromal cells. The proteins can exhibit cytokine, cell proliferation, or
CC cell differentiation activity (either inducing or inhibiting). They can

CC be used to support colony forming cells or factor-dependent cell lines,
CC to regulate hematopoiesis, and to treat myeloid or lymphoid cell
CC deficiencies. In addition, they may be used to support the growth and
CC proliferation of erythroid progenitor cells, and to treat various
CC anaemias. They can have colony stimulating factor (CSF) activity and can
CC be used to support the growth and proliferation of myeloid cells such as
CC granulocytes, monocytes or macrophages, to prevent or treat myelo-
CC suppression, to support the growth and proliferation of megakaryocytes
CC and platelets, thereby allowing prevention or treatment of platelet
CC disorders such as thrombocytopenia, to support the growth and
CC proliferation of hematopoietic stem cells, either in place of or in
CC conjunction with platelet transfusions, to treat stem cell disorders,
CC such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to
CC repopulate the stem cell compartment after irradiation or chemotherapy.
CC They can be used for growth or differentiation of bone, cartilage, and
CC tendon, ligament, or nerve tissue, as well as for wound healing and
CC tissue repair and replacement, and in the treatment of burns, incisions
CC and ulcers, to induce cartilage and/or bone growth in circumstances where
CC bone is not normally formed and thus have an application in healing bone
CC fractures and cartilage damage or defects, prophylactic use in fracture
CC reduction and also in the improved fixation of artificial joints
XX
XX
SQ Sequence 373 AA;

Query Match 99.1%; Score 1833.8; DB 3; Length 373;
Best Local Similarity 96.5%; Pred. No. 9.7e-65;
Matches 360; Conservative 0; Mismatches 1; Indels 12; Gaps 1;
QY 1 MEDLDQSLVSSDPPRPQPAFKYQFVREPEDEDEDEDEDEDEDELEVLKPA 60
DB 1 MEDLDQSLVSSDPPRPQPAFKYQFVREPEDEDEDEDEDEDEDELEVLKPA 60
QY 61 AGLSAAVPPTAPAGALMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
DB 61 AGLSAAVPPTAPAGALMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
QY 121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSQAEVPTVPAPAAPPPST 173
DB 121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSQAEVPTVPAPAAPPPST 173
QY 174 -----VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSYATIALLSVTISFRIYKG 228
DB 174 -----VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSYATIALLSVTISFRIYKG 228
QY 229 VIQAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNCCTIKELRRLFLVDDLVDSL 288
DB 241 VIQAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNCCTIKELRRLFLVDDLVDSL 300
QY 289 KFAVLMWVFTYVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAWAK 348
DB 301 KFAVLMWVFTYVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAWAK 360
QY 349 IQAKIPGLKRAE 361
DB 361 IQAKIPGLKRAE 373

RESULT 2
AAV56969
ID AAV56969 standard; protein; 373 AA.
XX
XX AAV56969;
XX
XX 25-APR-2000 (first entry)
XX Human MAGI polypeptide variant.
XX
XX MAGI protein; neuroendocrine-specific protein; neuropathy; human;
KW spinal injury; neuronal degeneration; neuromuscular disorder; cancer;
KW psychiatric disorder; developmental disorder; inflammatory disorder;
XX stroke; cytostatic; cerebroprotective; neuroprotective; variant.
OS Homo sapiens.

XX WO200005364-A1.
XX
XX 03-FEB-2000.
PD
XX 21-JUL-1999; 99WO-GB002360.
XX
XX 22-JUL-1998; 98GB-00016024.
PR 19-JUL-1999; 99GB-00016898.
XX
XX (SMIK) SMITHKLINE BEECHAM PLC.
XX
XX Michalovich D, Prinjha RK;
XX
XX WPI; 2000-182693/16.
DR N-FSDB; AAZ56888.
XX
XX Novel polypeptides related to neuroendocrine-specific proteins and
PT polynucleotides useful for diagnosis of various diseases and for
PT treatment of cancer and neurological disorders.
XX
XX Claim 2; Page 22; 35pp; English.
XX
XX The invention relates to human MAGI protein, which is similar to
CC neuroendocrine-specific protein. The MAGI protein can be expressed by
CC standard recombinant methodology. The MAGI polypeptides, polynucleotides
CC and antibodies are useful for treating diseases, including neuropathies,
CC spinal injury, neuronal degeneration, neuromuscular disorders,
CC psychiatric disorders and developmental disorders, cancer, stroke and
CC inflammatory disorders. The polynucleotide is also useful for chromosome
CC localization and for tissue expression studies. The present sequence
CC represents the human MAGI protein variant
XX
XX Sequence 373 AA;

Query Match 99.1%; Score 1833.8; DB 3; Length 373;
Best Local Similarity 96.5%; Pred. No. 9.7e-65;
Matches 360; Conservative 0; Mismatches 1; Indels 12; Gaps 1;
QY 1 MEDLDQSLVSSDPPRPQPAFKYQFVREPEDEDEDEDEDEDELEVLKPA 60
DB 1 MEDLDQSLVSSDPPRPQPAFKYQFVREPEDEDEDEDEDEDELEVLKPA 60
QY 61 AGLSAAVPPTAPAGALMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
DB 61 AGLSAAVPPTAPAGALMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
QY 121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSQAEVPTVPAPAAPPPST 173
DB 121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSQAEVPTVPAPAAPPPST 173
QY 174 -----VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSYATIALLSVTISFRIYKG 228
DB 174 -----VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSYATIALLSVTISFRIYKG 228
QY 229 VIQAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNCCTIKELRRLFLVDDLVDSL 288
DB 241 VIQAIQKSDGHPFRAYLESEVAISEELVQKYSNLSALGHVNCCTIKELRRLFLVDDLVDSL 300
QY 289 KFAVLMWVFTYVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAWAK 348
DB 301 KFAVLMWVFTYVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAWAK 360
QY 349 IQAKIPGLKRAE 361
DB 361 IQAKIPGLKRAE 373
RESULT 3
AAB24242
ID AAB24242 standard; protein; 373 AA.
XX
XX AAB24242;

Qy	61	AGLSAAPVETAPAAAGAPLMDFGNDVPVPAPPRGPIPAAPPVAPERQSPWDSPSVSTVPAP	120
Dd	61	AGLSAAPVETAPAAAGAPLMDFGNDVPVPAPPRGPIPAAPPVAPERQSPWDSPSVSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPASPVSQAEPVWTPPAPAPAAPBST-	173
Dd	121	SPLSAAAVSPSKLPEDDEPPARPPPPPASPVSQAEPVWTPPAPAPAAPBSTPAPAKRG	180
Qy	174	-----YVDLLYYWRDKKTGWVGASFLFLLLSLVFSIVSVTAYIALALLSVTSIFRIYG	228
Dd	181	SSGSVVVDLLYYWRDKKTGWVGASFLFLLLSLVFSIVSVTAYIALALLSVTSIFRIYG	240
Qy	229	VIOAIQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLDVSL	288
Dd	241	VIOAIQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLDVSL	300
Qy	289	KPAVLMMWVTYYGALFNGLTLILIALISLFSVPVIYERHQADIDHYLGANKVKDAMAK	348
Dd	301	KPAVLMMWVTYYGALFNGLTLILIALISLFSVPVIYERHQADIDHYLGANKVKDAMAK	360
Qy	349	IOAKIPGLKRKAEP	361
Dd	361	IOAKIPGLKRKAEP	373

RESULT 5	
AA047954	AA047954 standard; protein; 373 AA.
XX	
XX	
XX	AA047954;
XX	
XX	04-MAR-2002 (first entry)
XX	
XX	Human RTN4B SEQ ID NO 4.
XX	
XX	Human; RTN4B.
XX	
XX	Homo sapiens.
XX	
XX	CN1311439-A.
XX	
XX	05-SEP-2001.
XX	
XX	02-MAR-2000; 2000CN-00111791.
XX	
XX	02-MAR-2000; 2000CN-00111791.
XX	
XX	(UYFU-) UNIV FUDAN.
XX	
XX	Yu L, Fu Q, Zhao Y;
XX	
XX	WPI; 2002-049934/07.
XX	
XX	N-PSDB; ABA05903.
XX	
XX	Human RTN 4B protein and coding sequence, its preparation and use.
XX	
XX	Claim 5; Page 11 (Disclosure); 27pp; Chinese.
PS	

Db	1	MEDLQDSPLVSSSDUSPPAPQAFKQFVRPEDEDEDEDEDEDEDELEELERKPA	60
Qy	61	AGLSAAPVPTAPAAAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQSPWDPSPVSSSTVPAP	120
Db	61	AGLSAAPVPTAPAAAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQSPWDPSPVSSSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSQAEPPVTPPAPAPAAPSTSS	173
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSQAEPPVTPPAPAPAAPSTSPAAPKRRG	180
Qy	174	-----VDLLWYRDIKKTGVVFGASLFLLLSLTVFSIVSVTAVIALALLSVTISFRIYKG	228
Db	181	SSGSVVVDLLWYRDIKKTGVVFGASLFLLLSLTVFSIVSVTAVIALALLSVTISFRIYKG	240
Qy	229	VIQAIQKSDGEGHPPRAYLESEVAJISEELVOKYSNSALGHVNCITIKELRRLFLVDDLDVDSL	288
Db	241	VIQAIQKSDGEGHPPRAYLESEVAJISEELVOKYSNSALGHVNCITIKELRRLFLVDDLDVDSL	300
Qy	289	KEAVLMMVTVYVGALFNGLTLLILLALISLFSVPVIYERHOAQIDHYLGLANKNVKDAMAK	348
Db	301	KEAVLMMVTVYVGALFNGLTLLILLALISLFSVPVIYERHOAQIDHYLGLANKNVKDAMAK	360
Qy	349	IOAKTIGLKRKAE	361
Db	361	IOAKTIGLKRKAE	373

RESULT 6	
ABP68601	
ID	ABP68601 standard; protein; 373 AA.
XX	
AC	ABP68601;
XX	
DT	14-JAN-2003 (first entry)
XX	
DE	Human pancreatic cancer expressed protein SEQ ID NO 72.
DE	
XX	
KW	Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW	cytostatic; tumour.
XX	
OS	Homo sapiens.
XX	
PN	WO2002603117-A2.
XX	
PD	08-AUG-2002.
XX	
PF	30-JAN-2002; 2002WO-US002781.
XX	
PR	30-JAN-2001; 2001US-0265305P.
PR	31-JAN-2001; 2001US-0265682P.
PR	09-FEB-2001; 2001US-0267568P.
PR	21-MAR-2001; 2001US-0278651P.
PR	28-APR-2001; 2001US-0287112P.
PR	16-MAY-2001; 2001US-0291631P.
PR	12-JUL-2001; 2001US-0305484P.
PR	20-AUG-2001; 2001US-0313999P.
PR	27-NOV-2001; 2001US-0333626P.
XX	
PA	(CORI-) CORIXA CORP.
XX	
PI	Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
XX	
XX	WPI; 2002-627435/67.
DR	N-PSDB; ABV94681.
XX	
PT	New isolated polynucleotide and pancreatic tumor polypeptides, useful for
PT	diagnosing, preventing and/or treating cancer, particularly pancreatic
PT	cancer.
XX	
PS	Claim 2; SEQ ID NO 72; 300pp + Sequence Listing; English.
XX	
CC	The invention relates to an isolated polynucleotide (I) comprising: (a)
CC	any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)

complements of (a); (c) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridize to (a), under moderately stringent conditions; (e) sequences having at least 75% or 90% identity to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer in a patient and compositions comprising polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating pancreatic cancer and stimulating an immune response. The polynucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in the tumour cells, in vaccines and for gene therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo/pub/wipo/published_pct_sequences](http://pub/wipo/published_pct_sequences)

Query Match 99.1%; Score 1833.8; DB 5; Length 373;
Best Local Similarity 96.5%; Pred. No. 9.7e-65;
Matches 360; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

Qy	1	MEDLDQSPVSSSDSPRPQPAFKYQFVREPEDEEEEEEEDEDELEBLEVLERKPA	60
Dd	1	MEDLDQSPVSSSDSPRPQPAFKYQFVREPEDEEEEEEEDEDELEBLEVLERKPA	60
Qy	61	AGLSAAVPVPTAPAGAALMDFGNDVPPAPRGPLPAAAPPAPERQSPNDPSPVSSTVPAP	120
Dd	61	AGLSAAVPVPTAPAGAALMDFGNDVPPAPRGPLPAAAPPAPERQSPNDPSPVSSTVPAP	120
Qy	121	SPLSAAA VSPSKLPEDDEPPARP PPPPASVSPQAEPVMTTPAPAPAAPPSTTS	173
Dd	121	SPLSAAA VSPSKLPEDDEPPARP PPPPASVSPQAEPVMTTPAPAPAAPPSTPAAPKRGG	180
Qy	174	-----VDLLWROI KKTGVFGASLFLLLSLTVFSIVSVTAYITALALLSVTISPRIYKG	228
Dd	181	SSGSVVDDLLWROI KKTGVFGASLFLLLSLTVFSIVSVTAYITALALLSVTISPRIYKG	240
Qy	229	VIOAI OKSDEGHPFRAYLESEVAISEELAVOKYSNSALGHVNCTIKELRRLFLVDDLVDSL	288
Dd	241	VIOAI OKSDEGHPFRAYLESEVAISEELAVOKYSNSALGHVNCTIKELRRLFLVDDLVDSL	300
Qy	289	KFAVLMMVFTVVGALFNGLTLILLIALISLFSVPVIYERHQIQIDHYLGANKNVKDAMAK	348
Dd	301	KFAVLMMVFTVVGALFNGLTLILLIALISLFSVPVIYERHQIQIDHYLGANKNVKDAMAK	360
Qy	349	IOAKIPGLKKRAE	361
Dd	361	IOAKIPGLKKRAE	373

RESULT 7
ABB81079
ID ABB81079 standard; protein; 373 AA.

AC ABB81079;

AA
DT 05-NOV-2002 (first entry)

Human neurotransmitter receptor protein Nogo-B;

Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
KW
KW central nervous system; peripheral nervous system; tranquilizer; Nogo;
KW
KW vulnary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
KW
KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
KW
KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
KW
KW neurotransmitter receptor; human; receptor.

XX OS Homo sapiens.

XX
PN
US2002072493-A1

XX PD 13-JUN-2002.

XX	28-JUN-2001;	2001US-00893348.
PF	19-MAY-1998;	98IL-00124500.
XX	21-JUL-1998;	98MO-US014715.
PR	21-JUL-1998;	98MO-US014715.
PR	22-DEC-1998;	98US-00218277.
PR	19-MAY-1999;	99US-00314161.
XX	(YEDA)	YEDA RES & DEV CO LTD.
PA	Eisenbach-Schwartz M,	Hauben
XX	Moalem G;	
PI	WPI;	2002-607255/65.
PI	N-PSDB;	ABN86601.
XX		
DR		
DR		

Promoting nerve regeneration and preventing neuronal degeneration in the central/peripheral nervous system from injury/disease, comprises administering nervous system-specific activated T cells/antigen, or analogs/peptides.

PS Example; Page 56-57; 93pp; English.

The invention relates to promoting nerve regeneration or conferring neuroprotection and preventing or inhibiting neuronal degeneration in the central/peripheral nervous system (NS). The method involves administering NS-specific activated T cells, NS-specific antigen, its analogue or its peptide, a nucleotide sequence the NS-specific antigen or its analogue or combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, where the injury is spinal cord injury, blunt trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or damages caused by surgery such as tumour excision. The disease is not autoimmune disease or neoplasm. The disease results in a degenerative process occurring in either gray or white matter or both. The disease is diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, amyotrophic lateral sclerosis, non-artertic optic neuropathy, and vitamin deficiency, intervertebral disc herniation, prion diseases such as Creutzfeldt-Jakob disease, carpal tunnel syndrome peripheral neuropathies associated with various diseases, including but not limited to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary amyloidosis, obstructive lung diseases, acromegaly, malabsorption syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-pathies, complications of various drugs (e.g., metronidazole) and toxins (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia telangiectasia, Friedreich's ataxia, amyloid polynuropathies, adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's disease, or lipoproteinemia. The present sequence represents the human neurotransmitter receptor protein Nogo-66, an example of NS-specific antigen

Sequence 373 AA;

Query Match 99.1%; Score 1833.8; DB 5; Length 373;
Best Local Similarity 96.5%; Pred. No. 9.7e-65;
Matches 360; Conservative 0; Mismatches 1; Indels 12;

[illegible]

Dd 181 SSGSVVLLYYWRDIKKTGVFGASLFLLLSLTVFSVSVTVIAYIALALLSVTISFRIYKG 240

Qy 229 VIQAIQKSDGHPFRAYLESEVAISEELVOKYSNLSALGHVNCITIKELRRLFLVDDVLSL 288

Dd 241 VIQAIQKSDGHPFRAYLESEVAISEELVOKYSNLSALGHVNCITIKELRRLFLVDDVLSL 300

Qy 289 KFAVLMMVFTYVVGALFNGLTLLILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDMAMAK 348

Dd 301 KFAVLMMVFTYVVGALFNGLTLLILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDMAMAK 360

Qy 349 IQAKIPGLKRAE 361

Dd 361 IQAKIPGLKRAE 373

RESULT 8

ADI63044

ID ADI63044 standard; protein; 373 AA.

XX AC ADI63044;

XX DT 22-APR-2004 (first entry)

XX DE Human apoptosis-associated protein SEQ ID 487.

XX KW apoptosis; cell death; cytostatic; neuroprotective; immunosuppressive;

XX KW antirheumatic; antiarthritic; dermatological; antiinflammatory;

XX KW hepatotropic; virucide; nootropic; anticonvulsant; antiparkinsonian;

XX KW vasotropic; cerebroprotective; antialcoholic; gene therapy; tumour;

XX KW autoimmune disease; degenerative disease; viral infection; leukaemia;

XX KW carcinoma; sarcoma; multiple sclerosis; rheumatoid arthritis; diabetes;

XX KW lupus; hepatitis; influenza viruses; Alzheimer's disease;

XX KW Huntington's disease; Parkinson's diseases; reperfusion injury; stroke;

XX KW alcoholic liver disease; human.

XX OS Homo sapiens.

XX PN WO2003058021-A2.

XX PD 17-JUL-2003.

XX PF 13-JAN-2003; 2003WO-EP000270.

XX PR 11-JAN-2002; 2002DE-01000856.

XX PA (XANT-) XANTOS BIOMEDICINE AG.

XX PI Koenig-Hoffman K, Kazinski M, Schaefer R, Kesper B;

XX DR WPI; 2003-542134/51.

XX PT New nucleic acids involved in apoptosis, useful for diagnosis and

XX PT treatment of e.g. tumors and degenerative disease, also related proteins,

XX PT antibodies and modulators.

XX PS Claim 1b; SEQ ID NO 487; 517pp; German.

XX CC This invention describes novel nucleic acid molecules that are associated

XX CC with apoptosis and encode a polypeptide and are derived from a normalised

XX CC gene library (embryonic or liver) or clone collections, and the extent of

XX CC apoptosis measured by cell death detection assay or the CPRG assay

XX CC (measuring loss of membrane integrity). The products of the invention

XX CC have cytostatic, neuroprotective, immunosuppressive, antirheumatic,

XX CC antiarthritic, dermatological, antiinflammatory, hepatotropic, virucide,

XX CC nootropic, anticonvulsant, antiparkinsonian, vasotropic,

XX CC cerebroprotective and antialcoholic activity and can be used for gene

XX CC therapy. The polynucleotides also related vectors, hosts (or their

XX CC extracts), encoded polypeptide (or their receptors) and/or agents that

XX CC inhibit their activity (including antisense sequences) are used for

XX CC treatment or prevention of tumours, autoimmune or degenerative diseases

XX CC and viral infections, specifically leukaemia, carcinoma, sarcoma,

XX CC multiple sclerosis, rheumatoid arthritis, diabetes, lupus, or infection

XX CC with hepatitis or influenza viruses, Alzheimer's, Huntington's or

CC Parkinson's diseases, reperfusion injury, stroke and alcoholic liver

CC disease. Detection of the polynucleotides and derived polypeptides can

CC also be used for diagnosis of these diseases. This sequence represents an

CC apoptosis-associated protein described in the invention.

XX SQ Sequence 373 AA;

Query Match 99.1%; Score 1833.8; DB 7; Length 373;

Best Local Similarity 96.5%; Pred. No. 9.7e-65;

Matches 360; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

Qy 1 MEDLDQSPLVSSSDSPRPQPAFKYQFVREPEDEEEDEDEDELEEVLERKPA 60

Dd 1 MEDLDQSPLVSSSDSPRPQPAFKYQFVREPEDEEEDEDEDELEEVLERKPA 60

Qy 61 AGLSNAAPVPTAPAGAPLMDFGNDVFPAPRGPLPAAAPPVAPERQSPWDPSPVSTVPAP 120

Dd 61 AGLSNAAPVPTAPAGAPLMDFGNDVFPAPRGPLPAAAPPVAPERQSPWDPSPVSTVPAP 120

Qy 121 SPLSAAAVSPSKLPEDDEPPARPPPPASVSPOAEPVMTTPAPAPAAPPGTS----- 173

Dd 121 SPLSAAAVSPSKLPEDDEPPARPPPPASVSPOAEPVMTTPAPAPAAPPGTS----- 173

Qy 174 -----VDLLYWRDIKKTGVFGASLFLLLSLTVFSVSVTVIAYIALALLSVTISFRIYKG 228

Dd 181 SSGSVVLLYYWRDIKKTGVFGASLFLLLSLTVFSVSVTVIAYIALALLSVTISFRIYKG 240

Qy 229 VIQAIQKSDGHPFRAYLESEVAISEELVOKYSNLSALGHVNCITIKELRRLFLVDDVLSL 288

Dd 241 VIQAIQKSDGHPFRAYLESEVAISEELVOKYSNLSALGHVNCITIKELRRLFLVDDVLSL 300

Qy 289 KFAVLMMVFTYVVGALFNGLTLLILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDMAMAK 348

Dd 301 KFAVLMMVFTYVVGALFNGLTLLILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDMAMAK 360

Qy 349 IQAKIPGLKRAE 361

Dd 361 IQAKIPGLKRAE 373

RESULT 9

ADK67503

ID ADK67503 standard; protein; 373 AA.

XX AC ADK67503;

XX DT 06-MAY-2004 (first entry)

XX DE Human RTN-4B protein.

XX KW neuroprotective; gene therapy; BACE1 activity; RTN4; RTN3; amyloidosis;

XX KW Alzheimer's disease.

XX OS Homo sapiens.

XX PN WO2003089926-A2.

XX PD 30-OCT-2003.

XX PF 08-APR-2003; 2003WO-US000829.

XX PR 17-APR-2002; 2002US-0373284P.

XX PA (PHAA) PHARMACIA & UPJOHN CO.

XX PI Yan R, Lu Y;

XX DR WPI; 2003-854033/79.

XX PT New polypeptide having BACE1 activity, useful in preparing a composition

XX PT for treating amyloidosis or Alzheimer's disease.

XX PS Claim 52; SEQ ID NO 8; 42pp; English.

Peptide 180. .193
/note= "Nogob (ASV) peptide, distinguishes Nogob from
other Nogob isoforms"
Peptide 272. .285
/note= "Nogob (ASV) peptide"
WO200257483-A2.
25-JUL-2002.
18-JAN-2002; 2002WO-GB000228.
18-JAN-2001; 2001GB-00001312.
(GLAX) GLAXO GROUP LTD.
(SMIK) SMITHKLINE BEECHAM PLC.
Blackstock WP, Hale RS, Prinjha R, Rowley A;
WPI; 2002-599722/64.
N-PSDB; ABK90133.
Identifying modulators of Nogo or BACE activity for treating acute
neural injuries, neoplastic or dysproliferative disorders, comprises
providing and monitoring interaction between Nogo and BACE polypeptides.
Example 1; Page 25; 68pp; English.
The present invention relates to a new method of identifying modulators
of Nogo function or BACE activity. The method involves providing Nogo and
BACE polypeptides capable of binding with each other, monitoring the
interaction between these polypeptides, and determining if the test agent
is a modulator of Nogo or BACE activity. The method is useful in treating
acute neuronal injuries, such as spinal or head injury, stroke,
peripheral nerve damage, and in neoplastic (e.g. glioblastomas,
neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.
cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue
hypertrophy) of the central nervous system. The BACE polypeptide is
useful in screening methods to identify agents that may act as modulators
of BACE activity and in particular agents that may be useful in treating
Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,
and the polynucleotide encoding the BACE polypeptide are useful in
manufacturing a medicament for the treatment or prevention of disorders
responsive to the modulation of Nogo activity, in alleviating the
symptoms or improving the condition of a patient suffering from this
disorder, in axon regeneration, or in preventing metastasis or spreading
of a cancer. The polynucleotide may also be an essential component in
assays, a probe, in recombinant protein synthesis, and in gene therapy
techniques. The present amino acid sequence represents the human Nogob
protein of the invention
Sequence 373 AA;
Query Match 98.7%; Score 1825.8; DB 5; Length 373;
Best Local Similarity 96.0%; Pred. No. 28-64;
Matches 358; Conservative 1; Mismatches 2; Indels 12; Gaps 1;
QY 1 MEDLDQSLVSSDSSPPRPQAPFKYQFVREPEDEDEDEDEDEDEDELEVLKPA 60
DB 1 MEDLDQSLVSSDSSPPRPQAPFKYQFVREPEDEDEDEDEDEDELEVLKPA 60
QY 61 AGLSAAVPTAPAAAGAPLMDFGNDFVPPAPRGFLPAAPVAPERPSPVSTVPAP 120
DB 61 AGLSAAVPTAPAAAGAPLMDFGNDFVPPAPRGFLPAAPVAPERPSPVSTVPAP 120
QY 121 SPLSAAVSPSKLPBDEPPAPPPPPASVSPQAPVWTPPAPAPAPPPST----- 173
DB 121 SPLSAAVSPSKLPQDDEPPAPPPPPASVSPQAPVWTPPAPAPAPPPSTPAAPKRRG 180
QY 174 -----VVDLLYRDIKKTGVGASLFLLLSLTIVSVTVAYIALLLSVTSIRIYKG 228
DB 181 SSGSVVDLLYRDIKKTGVGASLFLLLSLTIVSVTVAYIALLLSVTSIRIYKG 240

QY 229 VIQAIQKSDGEPFRAYLESEVAISEELVQKYSNSALGHVNCIKELRRFLVDDLVDSL 288
DB 241 VIQAIQKSDGEPFRAYLESEVAISEELVQKYSNSALGHVNCIKELRRFLVDDLVDSL 300
QY 289 KPAVLMMVFTYVGALFNGLTLLILALISLFSVPVIYERHQAIIDHYLGANKNVKDAWAK 348
DB 301 KPAVLMMVFTYVGALFNGLTLLILALISLFSVPVIYERHQAIIDHYLGANKNVKDAWAK 360
QY 349 IQAKIPGLKRAE 361
DB 361 IQAKIPGLKRAE 373
RESULT 12
AAV56967
ID AAV56967 standard; protein; 1192 AA.
XX
AC AAV56967;
XX
DT 25-APR-2000 (first entry)
XX
DE Human MAGI polypeptide.
XX
KW MAGI protein; neuroendocrine-specific protein; neuropathy; human;
spinal injury; neuronal degeneration; neuromuscular disorder; cancer;
psychiatric disorder; developmental disorder; inflammatory disorder;
stroke; cytostatic; cerebroprotective; neuroprotective.
XX
OS Homo sapiens.
XX
FN WO200005364-A1.
XX
PD 03-FEB-2000.
XX
PF 21-JUL-1999; 99WO-GB002360.
XX
PR 22-JUL-1998; 98GB-00016024.
PR 19-JUL-1999; 99GB-00016898.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Michalovich D, Prinjha RK;
XX
DR WPI; 2000-182693/16.
DR N-PSDB; AAZ56886.
XX
PT Novel polypeptides related to neuroendocrine-specific proteins and
polynucleotides useful for diagnosis of various diseases and for
treatment of cancer and neurological disorders.
XX
PS Claim 2; Page 20-21; 35pp; English.
XX
CC The invention relates to human MAGI protein, which is similar to
neuroendocrine-specific protein. The MAGI protein can be expressed by
standard recombinant methodology. The MAGI polypeptides, polynucleotides
and antibodies are useful for treating diseases, including neuropathies,
spinal injury, neuronal degeneration, neuromuscular disorders,
psychiatric disorders and developmental disorders, cancer, stroke and
inflammatory disorders. The polynucleotide is also useful for chromosome
localization and for tissue expression studies. The present sequence
represents the human MAGI protein
Sequence 1192 AA;
Query Match 95.0%; Score 1756.9; DB 3; Length 1192;
Best Local Similarity 30.3%; Pred. No. 8-56-61;
Matches 361; Conservative 0; Mismatches 0; Indels 831; Gaps 1;
QY 1 MEDLDQSLVSSDSSPPRPQAPFKYQFVREPEDEDEDEDEDEDELEVLKPA 60
DB 1 MEDLDQSLVSSDSSPPRPQAPFKYQFVREPEDEDEDEDEDELEVLKPA 60
QY 61 AGLSAAVPTAPAAAGAPLMDFGNDFVPPAPRGFLPAAPVAPERPSPVSTVPAP 120

Db 121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPAPAPAAPSTPAAPKRRG 180
QY 172 ----- 171
Db 181 SSGSVDETLFALPAASEPVIRSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPUSP 240
QY 172 ----- 171
Db 241 LSAASFKEHYLGNLSTVLPTGTLQENVSEASKEVSEKAKTLIDRLDTEFSELEYSEM 300
QY 172 ----- 171
Db 301 GSSFSVSPRAESAVIVANPREBIIIVKNKDEBEKLVSNILHQQELPTALTCLKVREDEV 360
QY 172 ----- 171
Db 361 SSEKAKDSFNEKRVAVEAPMRSEYADFPERVNEVKSKEDSMDLAAGKIESNLSKV 420
QY 172 ----- 171
Db 421 DKKCFADSLQTNHEKDSSESSNDTSFPSTPEGIKDRPGAYITCAPFPNPAATESIATNIF 480
QY 172 ----- 171
Db 481 PLLGDPTSENKTEKKIEBKAQIVTEKNTSTKSNPFLVAAQDSEDTVYTTDLNLTQVTE 540
QY 172 ----- 171
Db 541 EVVANMPEGLTDPDLVQACESELNEVTGKIAYETKMDLVQTSVWQESLSYPAAQLCPSP 600
QY 172 ----- 171
Db 601 ESEATPSPVLPIVMEAPLNSAVPSAGASVIQPSSPLEASSVNVYESIKHPENPPPV 660
QY 172 ----- 171
Db 661 EAMSVLKKVSGIKBEEKPENINAALQTEAPYISACDLIKETKLSAEPAPDFSYSE 720
QY 172 ----- 171
Db 721 MAKVQVPDPHSELVEDSSPDSEVDLFSDDSIQDPVQKQDVTMLVKESLTETSFESMI 780
QY 172 ----- 171
Db 781 EYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLOMEELSTAVY 840
QY 172 ----- 171
Db 841 SNDDLFIKSAQIRETETFSDDSPIEIIDEFPTLISKTDSPSKLAREYTDLEVSHKSEI 900
QY 172 ----- 171
Db 901 ANAPDAGSLPCTELPHDLSLKNIOPKVBEKISFSDDFSKNGSATSKVLLLPDVSALAT 960
QY 172 ----- 171
Db 961 QAEIESIVKPKVLVKEAEKLPDTEKEDRSPSAIFSALSSTSVVDLLYWDIKKTGV 1020
QY 190 FGASFLLLSLTVFSIVSTAYIALALLSVTISPRIYKGVIOAIQKSDGHPFRAYLSE 249
Db 1021 FGASFLLLSLTVFSIVSTAYIALALLSVTISPRIYKGVIOAIQKSDGHPFRAYLSE 1080
QY 250 VAISELVQKYSNLSALGHVNCITIKELRRLFLVDDLSLKPAVLWVFYVGCALFNGLTL 309
Db 1081 VAISELVQKYSNLSALGHVNCITIKELRRLFLVDDLSLKPAVLWVFYVGCALFNGLTL 1140
QY 310 LILALISLFSVPVIERHQADIDHYLGLANKNVKDMAKIOAKIPCLKEKAE 361
Db 1141 LILALISLFSVPVIERHQADIDHYLGLANKNVKDMAKIOAKIPCLKEKAE 1192

RESULT 14
AAU04591

ID AAU04591 standard; protein; 1192 AA.
AC AAU04591;
XX 26-SEP-2001 (first entry)
DT Human Nogo protein.
DE Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein;
KW cranial trauma; cerebral trauma; spinal cord injury; stroke;
KW demyelinating disease; multiple sclerosis; monophasia demyelination;
KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis;
KW Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy;
KW Pelizaeus-Merzbacher disease; Spongy degeneration; Alexander's disease;
KW Canavan's disease; metachromatic leukodystrophy; viral infection;
KW Krabbe's disease.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT Domain 1054..1119
FT /label= Lumenal_extracellular domain
FT /note= "This sequence is specifically claimed"
FT Peptide 1055..1094
FT /label= Pep1
FT /note= "Receptor binding inhibitory peptide. This
FT sequence is specifically claimed"
FT Peptide 1064..1088
FT /label= Pep2
FT /note= "Receptor binding inhibitory peptide. This
FT sequence is specifically claimed"
FT Peptide 1074..1098
FT /label= Pep3
FT /note= "Receptor binding inhibitory peptide. This
FT sequence is specifically claimed"
FT Peptide 1084..1108
FT /label= Pep4
FT /note= "Receptor binding inhibitory peptide. This
FT sequence is specifically claimed"
FT Peptide 1095..1119
FT /label= Pep5
FT /note= "Receptor binding inhibitory peptide. This
FT sequence is specifically claimed"
XX WO200151520-A2.
PN 19-JUL-2001.
XX 12-JAN-2001; 2001WO-US001041.
XX 12-JAN-2000; 2000US-0175707P.
PR 26-MAY-2000; 2000US-0207366P.
PR 29-SEP-2000; 2000US-0236378P.
XX (UYUA) UNIV YALE.
XX Strittmatter SM;
XX WPI; 2001-442138/47.
DR N-PSDB; AAS09453.
XX Novel Nogo receptor protein useful for identifying modulator of Nogo
PT protein or Nogo receptor protein, which is useful for treating central
PT nervous system disorders.
XX Example 1; Page 101-104; 109pp; English.
PS The sequence is the human Nogo protein, a 250kDa myelin-associated axon
XX growth inhibitor. The invention relates to the use of the nogo receptor,
CC nogo protein, their nucleic acids, vectors expressing them and antibodies
CC against them, to isolate agents which block nogo receptor mediated axonal
CC growth. The agent is useful for treating a central nervous system
CC disorder which is a result of cranial or cerebral trauma, spinal cord

CC	injury, stroke or a demyelinating disease selected from multiple sclerosis, monophasia demyelination, encephalomyelitis, multifocal,
CC	leukoencephalopathy, panencephalitis, Marchiafava-Bignami disease,
CC	pontine myelinolysis, adrenoleukodystrophy, Pelizaeus-Merzbacher disease,
CC	Spongy degeneration, Alexander's disease, Canavan's disease,
CC	metachromatic leukodystrophy, viral infection and Krabbe's disease
XX	
SQ	Sequence 1192 AA;
	Query Match 95.0%; Score 1756.9; DB 4; Length 1192;
	Best Local Similarity 30.3%; Pred. No. 8.5e-61;
	Matches 361; Conservative 0; Mismatches 0; Indels 831; Gaps 1
Qy	1 MEDLDOSPLVSSSDSPRPQPAFKYQFVREPEDEEEEDDEDLEBEVLERKPA 60
Dd	1 MEDLDOSPLVSSSDSPRPQPAFKYQFVREPEDEEEEDDEDLEBEVLERKPA 60
Qy	61 AGLSAAPVTATAAGAPLMDFGNDVPAPRGPLPAAAPPAPERQPSWDPVSSTVPAP 120
Dd	61 AGLSAAPVTATAAGAPLMDFGNDVPAPRGPLPAAAPPAPERQPSWDPVSSTVPAP 120
Qy	121 SPLSAAAVSPSKLPEDDEPPARPPPPPASPVSQAEPVTPPAPAAPAPS----- 171
Dd	121 SPLSAAAVSPSKLPEDDEPPARPPPPPASPVSQAEPVTPPAPAAPASTTAAPKRRG 180
Qy	172 ----- 171
Dd	181 SSGSVDETFLALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPFVLETTAASLPSLSP 240
Qy	172 ----- 171
Dd	241 LSNASFKEHYIGNLSTVLPTGTTLQENVNSASKEVSEKATLLIDRLTFEFELEYSEM 300
Qy	172 ----- 171
Dd	301 GSSFYSPKAESAVIVANPREIIIVKNKDEEEKLVNNI LHNQQLPTALTCLKVKEDVV 360
Qy	172 ----- 171
Dd	361 SSEKAKDSFNKRVAVEAPMREEYADFKPFVRWEVKDSKDSDLMAAGGKIENLESKV 420
Qy	172 ----- 171
Dd	421 DKKCFADSLSEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAVITCAPNPATRSIATNIF 480
Qy	172 ----- 171
Dd	481 PLLGGDPTSSENKTDEKKIEBKAQIVTEKNTSTKTSNPFLVAAQODSETDYVTTDNLTWKVTE 540
Qy	172 ----- 171
Dd	541 EVVANMPGLTPDLVQEACESELNEVTGTKIAYETKMDDLVTSEVMQESLYPAAQLCPSF 600
Qy	172 ----- 171
Dd	601 ESEATPSPVLVDIWMAEPLNSAVPSAGASVIQPSSSPLEASSVNYESI KHEPENPPYE 660
Qy	172 ----- 171
Dd	661 EAMSVSLKKVGIKEEIKEPENINAALQETAPVISIACDLIKETKL SASPADFDSDYSE 720
Qy	172 ----- 171
Dd	721 MAKVEQVPDHPHSELVEDSPDSEPVDLFDSDSIDPVPOQDETVMLVKESLTETSFSMI 780
Qy	172 ----- 171
Dd	781 EYENKEKLSALPPEGCKPYLESFKLSLDNTXDTLLPDDEVSTLSKKEKIPLOMEELSTAVY 840
Qy	172 ----- 171
Dd	841 SNDDLFISEAQIRETETEDSSPTEIIDEFPTLISSKTDTSFKSLAREYTDLEVSHKSEI 900

Qy	172	-----	171
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDPVSALAT	960
Qy	172	-----	189
Db	961	QAEIESIVKPKVLKKEAKKLPSDTEKEDRSPSAISFAELSKTSSVDLLLYWRDIKKTGVV	1020
Qy	190	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHFPRAVLESE	249
Db	1021	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHFPRAVLESE	1080
Qy	250	VAISEELVQKYSNSALGHVNNCTIKEIRRLRFLVDLDVDSLKFAVLMMVFTYVGALFNGLT	309
Db	1081	VAISEELVQKYSNSALGHVNNCTIKEIRRLRFLVDLDVDSLKFAVLMMVFTYVGALFNGLT	1140
Qy	310	LILALISLFSVPVIYERHQAIIDHYLGLANKNVKDAMAKIQAKIPGLKRAE	361
Db	1141	LILALISLFSVPVIYERHQAIIDHYLGLANKNVKDAMAKIQAKIPGLKRAE	1192
RESULT 15			
ABG30938			
ID	ABG30938 standard; protein; 1192 AA.		
XX	AC ABG30938;		
XX	21-OCT-2002 (first entry)		
DT	Human NogoA protein.		
DE			
XX	Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;		
KW	stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;		
KW	neuroblastoma; hyperproliferative disorder; dysproliferative disorder;		
KW	cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;		
KW	tissue hypertrophy; central nervous system; axon regeneration; NogoA;		
KW	Nogo-associated disease; metastasis.		
XX			
OS	Homo sapiens.		
XX			
FN	WO200257483-A2.		
XX			
PD	25-JUL-2002.		
XX			
PF	18-JAN-2002; 2002WO-GB000228.		
XX			
PR	18-JAN-2001; 2001GB-00001312.		
XX			
FA	(GLAXO) GLAXO GROUP LTD.		
PA	(SMIK) SMITHKLINE BEECHAM PLC.		
XX			
PI	Blackstock WP, Hale RS, Prinjha R, Rowley A;		
XX			
DR	WPI; 2002-599722/64.		
XX	N-ESDB; ABK90134.		
XX			
PT	Identifying modulators of Nogo or BACE activity for treating acute		
PT	neuronal injuries, neoplastic or dysproliferative disorders, comprises		
PT	providing and monitoring interaction between Nogo and BACE polypeptides.		
XX			
PS	Disclosure; Page 59-62; 68pp; English.		
XX			
CC	The present invention relates to a new method of identifying modulators		
CC	of Nogo function or BACE activity. The method involves providing Nogo and		
CC	BACE polypeptides capable of binding with each other, monitoring the		
CC	interaction between these polypeptides, and determining if the test agent		
CC	is a modulator of Nogo or BACE activity. The method is useful in treating		
CC	acute neuronal injuries, such as spinal or head injury, stroke,		
CC	peripheral nerve damage, and in neoplastic (e.g. glioblastomas,		
CC	neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.		
CC	cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue		
CC	hypertrophy) of the central nervous system. The BACE polypeptide is		
CC	useful in screening methods to identify agents that may act as modulators		

CC of BACE activity and in particular agents that may be useful in treating
CC Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,
CC and the polynucleotide encoding the BACE polypeptide are useful in
CC manufacturing a medicament for the treatment or prevention of disorders
CC responsive to the modulation of Nogo activity, in alleviating the
CC symptoms or improving the condition of a patient suffering from this
CC disorder, in axon regeneration, or in preventing metastasis or spreading
CC of a cancer. The polynucleotide may also be an essential component in
CC assays, a probe, in recombinant protein synthesis, and in gene therapy
CC techniques. The present amino acid sequence represents the human NogoA
CC protein of the invention
XX
SQ Sequence 1192 AA;
Query Match 95.0%; Score 1756.9; DB 5; Length 1192;
Best Local Similarity 30.3%; Pred. No. 8.5e-61;
Matches 361; Conservative 0; Mismatches 0; Indels 831; Gaps 1;
QY 1 MEDLQSPVSSSDSPRRPQPAFKYQFVREPEDEDEDEDEDEDEDELEEVLERKPA 60
Db 1 MEDLQSPVSSSDSPRRPQPAFKYQFVREPEDEDEDEDEDEDELEEVLERKPA 60
QY 61 AGLSAAPVPTAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQSPVSTVPAP 120
Db 61 AGLSAAPVPTAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQSPVSTVPAP 120
QY 121 SPLSAAVSPSKLPEDDEPPAPPPPPASVSPQAPVWTPPAPAPAPPS----- 171
Db 121 SPLSAAVSPSKLPEDDEPPAPPPPPASVSPQAPVWTPPAPAPAPPSPPAPAKRRG 180
QY 172 ----- 171
Db 181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQDFPSVLELTAASLPSLSP 240
QY 172 ----- 171
Db 241 LSAASFKEHYLGNLSTVLPTGTQENVSEASKEVSEKAKTLIDRLDTFSELEYSEM 300
QY 172 ----- 171
Db 301 GSSFVSFPAESAVIVANPREIIIVNKNDEBKLYSNILHNQBELPTALTCLKVEDEVV 360
QY 172 ----- 171
Db 361 SSEKAKDSFNEKRVAVEAPRMREYADKPFERVWEVKDSKEDSMDLAAGKIESNLESKV 420
QY 172 ----- 171
Db 421 DKCFADSLQTNHEKQSSNDSTSPSTPEGIKDRPGAYITCAPFPNPAATESIATNIF 480
QY 172 ----- 171
Db 481 PLLGDPTSENKTEKKIEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKYTE 540
QY 172 ----- 171
Db 541 EYVANMPEGLTDLVQACESELNEVTGKIAYETKMDLVQTSVMQESLYPAAQLCPSPF 600
QY 172 ----- 171
Db 601 EESEATPSVPLDIVMEAPLNSAVFSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE 660
QY 172 ----- 171
Db 661 EAMSVLKKVSGIKKEIKPENINAAQTEAPYISACDLIKETKLSAEPAPDFSDYSE 720
QY 172 ----- 171
Db 721 MAKVEQVPDHSVELVEDSSPDSEPDVDFSDDSIPDVQPKQDETVMVKESLTETSFESMI 780
QY 172 ----- 171
Db 781 EYENKEKLSALPPEGKPYLESFKLSLNDNTKTLPLDDEVSTLSKKKEKTLQMEELSTAVY 840

QY 172 ----- 171
Db 841 SNDDLFIISKEAQIRETETFSDDSSPIEIIDEPFTLISSKTDSPSKLAREVTDLEVSHKSEI 900
QY 172 ----- 171
Db 901 ANAPDAGSLPCTELPHDLNKLNIQPKVEEKISFSDDFSKNGSATSKVLLAPPDVSALAT 960
QY 172 -----TSVVDLLLYWRDIKKTGV 189
Db 961 QAETESIVKPKVLVKEAEKLPSTTEKEDRSPSAIFSALSKTSVVDLLYWRDIKKTGV 1020
QY 190 FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLSE 249
Db 1021 FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLSE 1080
QY 250 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSKFAVLMWVFTYVGALFNGTL 309
Db 1081 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSKFAVLMWVFTYVGALFNGTL 1140
QY 310 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKIPGLKRAE 361
Db 1141 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDMAKIOAKIPGLKRAE 1192

Search completed: June 23, 2005, 10:52:04
Job time : 118.158 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2005, 10:29:31 ; Search time 25.0347 Seconds
(without alignments)
1387.446 Million cell updates/sec

Title: US-09-830-972-29-FUSED
Perfect score: 1850
Sequence: 1 MEDLQSLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRAE 361

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.1

Searched: 283416 seqs, 96216763 residues 283416
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	827.7	44.7	776	2 A46583	neuroendocrine-spe
2	684.2	37.0	208	2 I60904	neuroendocrine-spe
3	666	36.0	267	2 A60021	tropomyosin-relate
4	454.3	24.6	2484	2 T26216	hypothetical prote
5	447	24.2	2607	2 T26215	hypothetical prote
6	353.5	19.1	222	2 T26213	hypothetical prote
7	275.1	14.9	1173	2 T31421	C-terminal domain-
8	266	14.4	1206	2 S24407	formin isoform IV
9	266	14.4	1468	2 S11515	formin - mouse
10	264.1	14.3	1058	2 T13286	cappuccino gene pr
11	262.4	14.2	1611	2 T13236	hypothetical prote
12	260.9	14.1	760	2 F86387	probable Pto kinase
13	257.1	13.9	3511	2 A59295	unconventional myo
14	256.5	13.9	1255	2 T31065	diaphanous protein
15	255.5	13.8	3530	2 A59266	unconventional myo
16	253.8	13.7	1132	2 A59098	MHC class III hist
17	253.6	13.7	1201	2 G86441	unknown protein [i
18	250.9	13.6	1100	2 JC8033	leukocyte formin p
19	250.4	13.5	880	2 D89756	protein T23E7.2b [
20	250	13.5	980	2 J54986	regulatory protein
21	247.7	13.4	1015	2 SC6552	DNA topoisomerase
22	247.5	13.4	731	2 B86369	hypothetical prote
23	247.3	13.4	980	2 G75523	probable cell divi
24	247.2	13.4	1047	2 A55617	masquerade precurs
25	247	13.4	2090	2 S26058	probable transform
26	244.8	13.2	1127	2 T32404	hypothetical prote
27	244.8	13.2	1375	2 S48375	hypothetical prote
28	243.6	13.2	1721	1 I38902	retinoblastoma bin
29	243.4	13.2	3938	2 T42761	Bassoon protein -

30	243.3	13.2	708	2 D96711	hypothetical prote
31	243.3	13.2	786	2 A35466	progesterone recep
32	243	13.1	907	2 E96636	hypothetical prote
33	242.9	13.1	1634	2 T26517	hypothetical prote
34	242.6	13.1	716	2 T26998	hypothetical prote
35	241.5	13.1	933	1 ORHUP	progesterone recep
36	239.2	12.9	449	2 S16748	proline-rich prote
37	239.1	12.9	930	2 A25923	progesterone recep
38	238.7	12.9	1706	2 I84499	zinc finger protei
39	238.3	12.9	3149	1 Q0BE8	BPLF1 protein - hu
40	237	12.8	1137	2 A86335	T20H2.9 protein -
41	236.9	12.8	710	2 D96728	hypothetical prote
42	236.7	12.8	2649	2 T51023	hypothetical prote
43	235.6	12.7	765	2 T49592	neurofilament trip
44	235.2	12.7	1953	2 S63244	BNIL protein - yea
45	235.1	12.7	534	2 S21961	proline-rich prote

ALIGNMENTS

RESULT 1

A46583
neuroendocrine-specific protein, splice form A - human
N:Contains: neuroendocrine-specific protein, splice form B
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C:Accession: A46583; I60903
R:Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Ve
J. Biol. Chem. 268, 13439-13447, 1993
A:Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spec
A:Reference number: A46583; MUID:93293865; PMID:7685762
A:Accession: A46583
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-776 <ROE1>
A:Cross-references: UNIPROT:Q16799; GB:I10333; NID:G307306; PIDN:AAA59950.1; PID:G307307
A:Accession: I60903
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 421-776 <ROE2>
A:Cross-references: GB:I10334; NID:G307308; PIDN:AAA59951.1; PID:G307309
C:Genetics:
A:Gene: GDB:RTN1; NSP
A:Cross-references: GDB:203968; OMIM:600865
A:Map position: 14q21-14q22

Query Match	44.7%;	Score	827.7;	DB 2;	Length	776;
Best Local Similarity	27.1%;	Pred. No.	4.8e-20;			
Matches	196;	Conservative	55;	Mismatches	89;	Indels 383; Gaps 17;
QY	6	QSPL	-----	9		
Db	70	QSPVAMEATAGVAGVSSAMDHFTTSKDGSCVTSLSIDICYPQSDSTVFTGILQK	129			
QY	10	-----VSSDSPRR-----POP-----	21			
	:	:	:	:	:	:
Db	130	ENGHVITSEPSBELTGPSPSLPDVPGIESRGLFSSDSGIEMTPAESTEVNKILADPLDQM	189			
QY	22	---AFKYQVVRPEDEEEDEDEDELE---	50			
	:	:	:	:	:	:
Db	190	KAEAYKIDITRPEVKVHQEHHPELEDKDLDFKNKDTISIKPEGVREPDKPAPVEGKI	249			
QY	51	-----ELE---	53			
	:	:	:	:	:	:
Db	250	IKDHLLSESTFAPYIDDLSEQRAPQITTPVKVITLITEPSVETTTQETPEKQDICKL	309			
QY	54	-----VLERKPAAGLS---	64			
	:	:	:	:	:	:
Db	310	PSPDVTPTVTVSEPEDDPSGSIPTPSSGTPESAESQKGSISEDELITAIKEAKGLSVE	369			
QY	65	----RAPV-----PTAPAGAPL-----	78			

Db 370 TAENPRVGLADRPVKARSGPPTIP-----SPLDHEASSAESGDSIELVSEDPMAAEDA 426
QY 79 -----MDFGNDFFPPAPRGLPRAAPV-----APE 103
Db 427 LPSGVYSGHVGGP-----PSPASPSIQYIILREARELDSELIIESCDASASESPK 482
QY 104 RQ---PSWDSPVVS-----STVPAPSPLSAAVSP 130
Db 483 REQDSPMPKPSALDAIREETGVRAERAPSRGLAEPGSLDYPSTEPQGP-----534
QY 131 SKLPED-----EPPARPPPPASVSPQAEVPWTPAP-APAAPP-----STSVDDL 178
Db 535 -ELPPDGDGALEPETMLPKPEEDSSNQSPAAATKGPGLGCPAPPLFLNKAIDLL 593
QY 179 YNRDIKKTGVFGASLFLLLSVTSVIVAYIALALLSVTISFRIYKGVIOAKSDE 238
Db 594 YNRDIKQTGIVFGSFLLLFSLTQFSVSVVAYIALAALSATISFRIYKSVIQAQVKTDE 653
QY 239 GHPPFRAYLESEVAISELQVYKYSNSALGHVNCITIKELRRLFLVDLVDLSLKFVLMWVFT 298
Db 654 GHPPFRAYLEITLSQEQIKYQKTDCLQFYVNSTKLRLFLVDLVDLSLKFVLMWLLT 713
QY 299 YVGALENGTLILALISLPSVPIYERHOAQIDHYGLANKNVKDMAKIOAKIPGLKR 358
Db 714 YVGALENGTLILMAVSMFTLPVVVYKHQAQIDQYGLVTRTHINAVVAKIOAKIPGAKR 773
QY 359 KAE 361
Db 774 HAE 776

RESULT 2
I60904
neuroendocrine-specific protein C - human
C:Species: Homo sapiens (man)
C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C:Accession: I60904
R:Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; V
J. Biol. Chem. 268, 13439-13447, 1993
A:Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spe
A:Reference number: A46583; MUID:93293865; PMID:7685762
A:Accession: I60904
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-208 <RES>
A:Cross-references: UNIPROT:Q16799; GB:L10335; NID:g307310; PIDN:AAAS9952.1; PID:g307311
C:Genetics:
A:Gene: GDB:RTN1; NSP
A:Cross-references: GDB:203969; OMIM:600865
A:Map position: 14q21-14q22

Query Match 37.0%; Score 684.2; DB 2; Length 208;
Best Local Similarity 62.4%; Pred. No. 1.3e-16;
Matches 131; Conservative 35; Mismatches 36; Indels 8; Gaps 1;
QY 152 SPOAEPVWTPAPAPAPSTSVVDLLYWRDIKKTGVFGASLFLLLSVTSVIVSTAY 211
Db 7 STKMDCVW-----SNWKSQAIDLLYWRDIKQTGIVFGSFLLLFSLTQFSVSVVAY 58
QY 212 IALALLSVTISFRIYKGVIOAKSDEGHPPFRAYLESEVAISELVQKYSNSALGHVNC 271
Db 59 LALAALSATISFRIYKSVLQAVQKTDGHPFRAYLEITLSQEQIKYQKTDCLQFYVNST 118
QY 272 IKELRRLFLVDLVDLSLKFVLMWVTVYVYVAYIALALLSVTISFRIYKGVIOAKS 331
Db 119 IKELRRLFLVDLVDLSLKFVLMWLLTYVYVAYIALALLSVTISFRIYKGVIOAKS 178
QY 332 DHYGLANKNVKDMAKIOAKIPGLKRKAE 361
Db 179 DQYGLVTRTHINAVVAKIOAKIPGAKRAE 208

RESULT 3

A60021
tropomyosin-related protein, neuronal - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Nov-1999
C:Accession: A60021
R:Wieczorek, D.F.; Hughes, S.R.
Brain Res. Mol. Brain Res. 10, 33-41, 1991
A:Title: Developmentally regulated cDNA expressed exclusively in neural tissue.
A:Reference number: A60021; MUID:91278684; PMID:1647480
A:Accession: A60021
A:Molecule type: mRNA
A:Residues: 1-267 <WIE>
A:Cross-references: EMBL:X52817; NID:g456549; PIDN:CAA37001.1; PID:g456550
C:Comment: This neuronal-specific mRNA was identified by hybridization to an alpha-tropo
Query Match 36.0%; Score 666; DB 2; Length 267;
Best Local Similarity 66.1%; Pred. No. 1e-15;
Matches 123; Conservative 34; Mismatches 29; Indels 0; Gaps 0;
QY 172 TSVVDLLYWRDIKKTGVFGASLFLLLSVTSVIVSTAYIALALLSVTISFRIYKGVIO 231
Db 10 SQAIDLLYWRDIKQTGIVFGSFLLLFSLTQFSVSVVAYIALAALSATISFRIYKSVIO 69
QY 232 AIQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDLVDLSL 291
Db 70 AVQKTDGHPFRAYLEITLSQEQIKYQKTDCLQFYVNSTKLRLFLVDLVDLSL 129
QY 292 VLMWVTVYVYVAYIALALLSVTSVIVSTAYIALALLSVTISFRIYKGVIOAKS 351
Db 130 VLMWLLTYVYVAYIALALLSVTISFRIYKGVIOAKS 189
QY 352 KIPGLK 357
Db 190 KIPGAR 195

RESULT 4
T26216
hypothetical protein W06A7.3c - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26216
R:Ainscough, R.
Submitted to the EMBL Data Library, August 1996
A:Reference number: Z20173
A:Accession: T26216
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2484 <WIL>
A:Cross-references: UNIPROT:Q9U347; EMBL:Z78066; PIDN:CAB51467.1; GSPDB:GN00023; CESP:W06A7
A:Experimental source: clone W06A7
C:Genetics:
A:Gene: CESP:W06A7.3c
A:Map position: 5
A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2
Query Match 24.6%; Score 454.3; DB 2; Length 2484;
Best Local Similarity 15.7%; Pred. No. 4.2e-06;
Matches 126; Conservative 79; Mismatches 142; Indels 457; Gaps 18;
QY 1 MEDLQSPSLVSSSDSPRR-----PQAFKIQYFV-----REPDEEEE 38
Db 1679 VESLERPLTIITQKPPKPTEDIGALSPLSNTLAEEVEVPMDMQSVPHSPQEQEEI 1738
QY 39 E-----EEE 42
Db 1739 EALSIIIEBPQAMKEVPESAPKDNESLEAPIINEPIRRLVETKIMGPKSLNED 1798
QY 43 EDEDED-----48
Db 1799 NDDDDGSECLSDIGLSERTIQRTNTSIDPSIRDSFSSISSFGDROKFRTAENIRQ 1858
QY 49 -----LEELEVLER 57

```
Db 1859 DLLPFQSSVSYLRSSPNFSQQLLVNLSMSPDLSNAPPVGVGFNTAQLFLEKQOEDR 1918
QY 58 KPAAG-----LSAAPV----- 68
Db 1919 PSAEGSIDSGGPEKVDHEGLDEFAAPPVHDPMQKSVFGSLGDDMKPGSQDDGFVFIERN 1978
QY 69 -----PTAPAGAPLM----- 79
Db 1979 EANEATLKKQKMSHHNDVIEKNYFNDAFTAALLESPIAEARKLVQDAVESASEYKK 2038
QY 80 -----DFGNDVFPPA----- 89
Db 2039 QAVSDGEIGRELLDNVEQKIEQVKPEIVDSLHKAYDGVGFVHETVPNAVDDFVREAEK 2098
QY 90 --PRGLP-----AAPP-----VAP--ERQP----- 106
Db 2099 QLPESVPKEIETPEPLVDIHTDKVHDEVNLFRRPTPPETDDVAPLSDDKPQFCN 2158
QY 107 -----SWDPSVSTVPAPSPLSAAAAPS 132
Db 2159 QTPEDDETTFRKGPIPTPEEVEKAAQNNLDLDDPLVTSNTGAAGAAVGAASAVES 2218
QY 133 LPEDD-----EPPARPPPP-----PASV-----SPOAEP-----V 158
Db 2219 LTEEMFGHQKFTVPRPTPKDISDEDKPSTVNLGSPSHHSHSPSSPHHSILKHGDA 2278
QY 159 W-----TPAPAPAPPSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIA 213
Db 2279 WIDFKTVPPC-----VLDVIYWRDAKSAIVLSLALLVFLVAKYPLLVTVVYSL 2328
QY 214 LALLSVTISFRIYKGVIOAKSDGHPFRAYLESEVAISEELVKQYSNLSALGHVNCITK 273
Db 2329 LLALGAAAGFRVFKVEAQIKKTDSEHPFSEILAQDLTLPOEKVHAQADVFEHATCIAN 2388
QY 274 ELRLPLVDLSDLKFAVLMVFTVVGALFNGLTLLIALLSLFSPVPIYERHQAIQIDH 333
Db 2389 KUKGLVFSPLSIEKFGVLMSLTVIASWFSGFTLAILGLLGVSFVKPYESNQEAIDP 2448
QY 334 YLGLANKVNDAMAKIOAKIPGLK 357
Db 2449 HLATISGHLKNVQNIIDEKLPFLR 2472
```

RESULT 5

T26215

hypoetical protein W06A7.3a - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T26215

R:Ainscough, R.

submitted to the EMBL Data Library, August 1996

A:Reference number: Z20173

A:Accession: T26215

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-2607 <WIL>

A:Cross-references: UNIPROT:Q23187; EMBL:Z78066; PIDN:CA01522.2; GSPDB:GN00023; CESP:W0

A:Experimental source: clone W06A7

C:Genetics:

A:Gene: CESP:W06A7.3a

A:Map position: 5

A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2; 2586/2

Query Match

Best Local Similarity 24.2%; Score 447; DB 2; Length 2607;

Matches 128; Conservative 79; Mismatches 150; Indels 560; Gaps 18;

QY 1 MEDLOSPLVSSSDSPRR-----PQAFKYOQV-----REPDEDEEE 38

Db 1679 VESLERPLTIITQKKPEKPTEDIGALSPISPTLAEYEVPMQVPMQSVPHSPQEQEII 1738

QY 39 E-----EEE 42

```
Db 1739 EALSELIEBPQAMKEVKEPVESAPEKDNESLEAPELINEPIRRLVETKIMGPGKSLNED 1798
QY 43 EDEDED----- 48
Db 1799 NDDDDSGSCLSDIGLDSERTIQRFNTSIDPSIRRDSPSSISFGDRQKFRTAENIRQ 1858
QY 49 -----LEELVLER 57
Db 1859 DLLPFQSSVSYLRSSPNFSQQLLVNLSMSPDLSNAPPVGVGFNTAQLFLEKQOEDR 1918
QY 58 KPAAG-----LSAAPV----- 68
Db 1919 PSAEGSIDSGGPEKVDHEGLDEFAAPPVHDPMQKSVFGSLGDDMKPGSQDDGFVFIERN 1978
QY 69 -----PTAPAGAPLM----- 79
Db 1979 EANEATLKKQKMSHHNDVIEKNYFNDAFTAALLESPIAEARKLVQDAVESASEYKK 2038
QY 80 -----DFGNDVFPPA----- 89
Db 2039 QAVSDGEIGRELLDNVEQKIEQVKPEIVDSLHKAYDGVGFVHETVPNAVDDFVREAEK 2098
QY 90 --PRGLP-----AAPP-----VAP--ERQP----- 106
Db 2099 QLPESVPKEIETPEPLVDIHTDKVHDEVNLFRRPTPPETDDVAPLSDDKPQFCN 2158
QY 107 -----SWDPSVSTVPAPSPLSAAAAPS 132
Db 2159 QTPEDDETTFRKGPIPTPEEVEKAAQNNLDLDDPLVTSNTGAAGAAVGAASAVES 2218
QY 133 LPEDD-----EPPARPPPP-----PASV-----SPOAEP-----V 158
Db 2219 LTEEMFGHQKFTVPRPTPKDISDEDKPSTVNLGSPSHHSHSPSSPHHSILKHGDA 2278
QY 159 W-----TPAPAPAPPSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIA 213
Db 2279 WIDFKTVPPC-----VLDVIYWRDAKSAIVLSLALLVFLVAKYPLLVTVVYSL 2328
QY 214 LALLSVTISFRIYKGVIOAKSDGHPFRAYLESEVAISEELVKQYSNLSALGHVNCITK 273
Db 2329 LLALGAAAGFRVFKVEAQIKKTDSEHPFSEILAQDLTLPOEKVHAQADVFEHATCIAN 2388
QY 274 ELRLPLVDLSDLKFAVLMVFTVVGALFNGLTLLIALLSLFSPVPIYERHQAIQIDH 333
Db 2389 KUKGLVFSPLSIEKFGVLMSLTVIASWFSGFTLAILGLLGVSFVKPYESNQEAIDP 2448
QY 334 YLGLANKVNDAMAKIOAKIPGLK 357
Db 2449 HLATISGHLKNVQNIIDEKLPFLR 2472
```

RESULT 6

T26213

hypoetical protein W06A7.3b - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T26213

R:Ainscough, R.

submitted to the EMBL Data Library, August 1996

A:Reference number: Z20173

A:Accession: T26213

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-222 <WIL>

A:Residues: 1-1206 <JAC>
A:Cross-references: UNIPROT:Q05859; EMBL:X62379; NID:G51552; PIDN:CAA4244.1; PID:G51553

Query Match 14.4%; Score 266; DB 2; Length 1206;
Best Local Similarity 17.3%; Pred. No. 1.7;
Matches 102; Conservative 40; Mismatches 97; Indels 350; Gaps 24;

QY 5 DQSPVSSSDSPR-----PQAFKQFVREPEDEE-----EEEE 41
DB 459 DQSPTEQDDRTGRLQAVWPPPKTK-----DTEKVLKYTEAYQAAILHLKREHK 510
QY 42 EDEE-----DEDLEEL-EVLERK----- 58
DB 511 EEIETLQAOFEKLTTHIRGEHALVTARLEAEIENLQOKEKREGCEMRDVCISTDDDC 570
QY 59 -PAA----- 61
DB 571 SPKAFRNVCITQDRETFKPCDAESKATRSSQIVPKKLTISLTQLSPSKSDKDIHAPFQT 630
QY 62 --GLSA-----APVETAPAGAPLMDFGNDFVPPAP-----RGPLPAPAPVAPERQ 105
DB 631 REGTSSSSQOKISPPAP-PTPPPLPPL-----IPPPPLPPLGGLPLPAPPPIPP--- 679
QY 106 PSWDPSVSTVPAPSPLSAAAASPSKLPEDDEPPARPPPPPPA-----SVSPQAE 157
DB 680 ----VCVPSPPPPPPP-----PPTVPSPDGPPPPPPPPPLPNVLPALPNSGGPPPP 729
QY 158 VMTPPAP--APAAPSTSV-----VDLLYMRDIKKTGVVFGASLF 195
DB 730 PPPPPPPGLAPPPPPGLSFGLSSSSSQYPRKPAIEPSCPMKPLYWTR----- 776
QY 196 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIOKSDGHP-----FRAY 245
DB 777 -----IQINDKSQDAAPTLDWDSLEEPHIRT 802
QY 246 LESEVAISEELVQ-----KYSNSA---LGHVNCITKELAR 277
DB 803 SEFEYLFSDTTOQKKKPLSEAYEKKNVKKIILKLDGKRSQTVGLISLHLEMDIQ 862
QY 278 -LFLVDLVDLSLKFAVLMVFTYVVGALFNGLTLILALISLSVPVYIERHOAIDHYLG 336
DB 863 AIFTVD-----SVVDLETALAYE----- 882
QY 337 LANKNVKDMAKIQ-----AKIPGLKRAE 361
DB 883 --NRAQEDLTIRKYETSKEDLKLDPQFHLHQAIPNFAERAQ 929

RESULT 9
S11515
formin - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S11515
R:Woychik, R.P.; Maas, R.L.; Zeller, R.; Vogt, T.F.; Leder, P.
Nature 346, 850-853, 1990
A:Title: 'Formins': proteins deduced from the alternative transcripts of the limb deform
A:Reference number: S11515; MUID:90363291; PMID:2392150
A:Accession: S11515
A:Molecule type: mRNA
A:Residues: 1-1468 <WOY>
A:Cross-references: UNIPROT:Q05860; EMBL:X53599; NID:G52877; PIDN:CAA37668.1; PID:G52878

Query Match 14.4%; Score 266; DB 2; Length 1468;
Best Local Similarity 17.3%; Pred. No. 2.8;
Matches 102; Conservative 40; Mismatches 97; Indels 350; Gaps 24;

QY 5 DQSPVSSSDSPR-----PQAFKQFVREPEDEE-----EEEE 41
DB 685 DQSPTEQDDRTGRLQAVWPPPKTK-----DTEKVLKYTEAYQAAILHLKREHK 736
QY 42 EDEE-----DEDLEEL-EVLERK----- 58

DB 737 EEIETLQAOFEKLTTHIRGEHALVTARLEAEIENLQOKEKREGCEMRDVCISTDDDC 796
QY 59 -PAA----- 61
DB 797 SPKAFRNVCITQDRETFKPCDAESKATRSSQIVPKKLTISLTQLSPSKSDKDIHAPFQT 856
QY 62 --GLSA-----APVETAPAGAPLMDFGNDFVPPAP-----RGPLPAPAPVAPERQ 105
DB 857 REGTSSSSQOKISPPAP-PTPPPLPPL-----IPPPPLPPLGGLPLPAPPPIPP--- 905
QY 106 PSWDPSVSTVPAPSPLSAAAASPSKLPEDDEPPARPPPPPPA-----SVSPQAE 157
DB 906 ----VCVPSPPPPPPP-----PPTVPSPDGPPPPPPPPPLPNVLPALPNSGGPPPP 955
QY 158 VMTPPAP--APAAPSTSV-----VDLLYMRDIKKTGVVFGASLF 195
DB 956 PPPPPPPGLAPPPPPGLSFGLSSSSSQYPRKPAIEPSCPMKPLYWTR----- 1002
QY 196 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAIOKSDGHP-----FRAY 245
DB 1003 -----IQINDKSQDAAPTLDWDSLEEPHIRT 1028
QY 246 LESEVAISEELVQ-----KYSNSA---LGHVNCITKELAR 277
DB 1029 SEFEYLFSDTTOQKKKPLSEAYEKKNVKKIILKLDGKRSQTVGLISLHLEMDIQ 1088
QY 278 -LFLVDLVDLSLKFAVLMVFTYVVGALFNGLTLILALISLSVPVYIERHOAIDHYLG 336
DB 1089 AIFTVD-----SVVDLETALAYE----- 1108
QY 337 LANKNVKDMAKIQ-----AKIPGLKRAE 361
DB 1109 --NRAQEDLTIRKYETSKEDLKLDPQFHLHQAIPNFAERAQ 1155

RESULT 10
T13286
cappuccino gene protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T13286
R:Emmons, S.; Phan, H.; Calley, J.; Chen, W.; James, B.; Manseau, L.
Genes Dev. 9, 2482-2494, 1995
A:Title: Cappuccino, a Drosophila maternal effect gene required for polarity of the egg
A:Reference number: T17651; MUID:96033799; PMID:7590229
A:Accession: T13286
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1058 <EMM>
A:Cross-references: UNIPROT:Q24120; EMBL:U34258; NID:G1061333; PID:G1061334; PIDN:AAC469;
C:Genetics:
A:Gene: capu
A:Cross-references: FlyBase:FBgn0000256

Query Match 14.3%; Score 264.1; DB 2; Length 1058;
Best Local Similarity 16.1%; Pred. No. 1.4;
Matches 118; Conservative 47; Mismatches 117; Indels 449; Gaps 27;

QY 9 LVSSSDSPR-----PQAFKQF-----VREPEDEEEEEEE--- 42
DB 398 LLSVDEPPRRSKRCVNLTELLNASEATVYENKTGAEGCVKSFDTAQTQISEDECGT 457
QY 43 -----EDEDELELEVLKPAAGLSAAPVTPAPAGAPLMDFGNDPV-PP 88
DB 458 CKQGSSTKVSNDKSAKEDGE-----KPHA--VAPPPPPPPPLPA-----EVAPP 501
QY 89 ARGPLPAPVAPERQSPSWDPSVSTVPAPSPLSAAAASPSKLPEDDEPPAR----- 142
DB 502 PPPPPPPPPPLANYGAP---PPP-----PPPPPGSGSAPP-----PPAPIEGGG 546
QY 143 -PPPPPPASVSPQAEV----- 160
DB 547 IPPPPPPPSASPSKTTISAPLPDPAEGNWFHRTNTRKSAVNPPKPMPLVYTRIVTSA 606

```
QY 161 PPAP-----APAAPPSTSVVDLLYWRDIKKT-----186
Db 607 PAPRPPSVANSTDSTENSGSPDEPPAANGADAPTAPATKEI-----WTIEETPLDN 662
QY 187 -----GVVF-----190
Db 663 IDEFTELFSRQAIAPVSKPKELKVKRAKSIKVLDPERSRNVGLIWRSLHVPSSSEIHAHY 722
QY 191 -----GASLFL-----LLSLTVFSI-----VSV 208
Db 723 HDTSVSVLEALQHSNIOATELQRIKEAAGGDIPLDHPQFLDLISLMSASERISC 782
QY 209 TAYIALALLSVTISFRIVKGVIOAIO-----234
Db 783 IVFOAEFESVILLFRKLTFTVSQLSQQLESDELKLVFSIILTLGNMNGNRQORQADG 842
QY 235 -----KSDRGH-----240
Db 843 FNLIDILGKLKDVKSKESTTLHLHFIVRTYIAQRKEGVHPLRLPIPEPADVERAAQMD 902
QY 241 -----PFRAYLSEVAISEELVQKYSNLSAL 265
Db 903 FEEVOQQIFDLNKKFLGCKRTTAKVLAASRPEIMEFFKSKMEEFVEGADKSMALHQSS--960
QY 266 GHVNCCTIKELRLFL-----VDDLVDLSLKFAVL 293
Db 961 -----LDECRDLFLETMRPFYHSPKACTLTLAQCTPDQFFYWTNFTNDFKDIWK-----1010
QY 294 MVFTYVVGALFNGLTLLILALISLFSVPVYIERHQADIDHYLGLANKNVKIDAMAK---IQ 350
Db 1011 -----KEITSLNELL-----MKSKQAQIE-----SRNVSTKVKSGRIS 1046
QY 351 AKIPGLKRAE 361
Db 1047 LKERMLMRRSK 1057

RESULT 11
T39236
hypothetical protein SPAC23A1.17 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T39236
R:Murphy, L.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, February 1998
A:Reference number: Z21780
A:Accession: T39236
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1611 <MUR>
A:Cross-references: UNIPROT:O42854; EMBL:AL021813; PTDN:CAAL6991.1; GSPDB:GN00066; SPDB:
A:Experimental source: strain 972h-; cosmid c23A1
C:Genetics:
A:Gene: SPDB:SPAC23A1.17
A:Map position: 1

Query Match 14.2%; Score 262.4; DB 2; Length 1611;
Best Local Similarity 9.8%; Pred.No. 4.6;
Matches 127; Conservative 57; Mismatches 112; Indels 1006; Gaps 29;

QY 2 EDL-----DOSPLV-----SSSDGSPRP-----19
Db 299 EELSKSRVAKDDPPVSVNTANSDEPSSSKPAKPLTDLNRASFQRLNLDQKPKCKSQG 358
QY 20 -----OPAKYQVREPDDEE-----EEEEEEDEDL 49
Db 359 EISEQEDEYDAAESDEMHSPTSTHEPESEPDQDEPSEKDKDENKQVEEQEQQEQQE 418
QY 50 EELE-----VLERKPAAG-----62
Db 419 DPEEKRIALRERMAKSGGIMHVFLGFLAIPGRKNTLRTPAKSSEAKSTTNDSS 478
```

```

Qy 293 -----LMVFTTVG---ALFNGLT----- 308
Db 554 KSSNILLENNPHALVSDFLAKLALDCNTHITTRVMGTFGYMAPEYASSGKLTSEKSDVFS 613
Qy 309 --LLILALIS-----LFSVPVIYERHQIIDIHYLG----- 336
Db 614 FGVLLELITGRKPDVASQPLGDESLSVEWAPRLSSNATETEEFTALADPKLGRNVGVGM 673
Qy 337 -----LANKNVKXDM-----AKIQAKIPCL 356
Db 674 FRMTEAAAACIRHSATKRPMSQIVRAPDLSAEEDLTNGMRLGSEIINSAAQSSAIRLF 733
Qy 357 KRKA 360
Db 734 RRMA 737

RESULT 13
A59295
unconventional myosin-15 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C:Accession: A59295
R:Liang, Y.; Wang, A.; Belyantseva, I.A.; Anderson, D.W.; Probst, F.J.; Barber,
an, T.B.; Fridell, R.A.
Genomics 61, 243-258, 1999
A>Title: Characterization of the human and mouse unconventional myosin XV genes
A:Reference number: A59266; MUID:20021762; PMID:10552926

```

```

A:Accession: A59295
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-3511 <LIA>
A:Cross-references: UNIPROT:Q9QZ4; GB:AFL44095; NID:g6224684; PIDN:AAF05904.1
C:Genetics:
A:Gene: MGI:Myo15
A:Cross-references: MGI:1261811
A:Map position: 11:33.9
F:1209-1871/Domain: myosin motor domain homology <MMO>

      Query Match      13.9%; Score 257.1; DB 2; Length 3511;
      Best Local Similarity 9.5%; Pred. No. 50;
      Matches 136; Conservative 46; Mismatches 113; Indels 1139; Gaps 35

Qy 16 PPRP-----QPAFKYQV-----REPDEEEE----- 37
Db 388 PGMEYVYPEPAFYWPVPPPIPSHPNPYAHPMDDIAELEPEETGEERQSTSRFLPSAA 447
Qy 38 -----EEEEEE-----EEEEEE 43
Db 448 FFEQGMKDPARSKLSIRKRLPRRQVKLFGKEKLEVPPLPSLDIPLPLGDAGESEE 507
Qy 44 DEDEDLELEVLKRPAGLSAAPVPTAP-----AAGAPL-MDF 81
Db 508 EE-----MPVPVTPYTHPYWSFLTQRNLQRLSALSFARQGLGF 548
Qy 82 GNDVPVPAPR-----GPLP-----AAPVVA----- 101
Db 549 GPEFGHTPRPATSLARFLKTLSEKXPIPLRGSQKARGGRPVREAAAYKRGYKLAGM 608
Qy 102 -PER-----QPSWDPS-----VSSTVPAPSPLSAAAVS 129
Db 609 DEDRPNTIVLRRSQPARNNNSHGPPSPRPAPRALTHWSALISPPMPAPSPSPASPLT 668
Qy 130 ----- 129
Db 669 PPSPTFSRPPRLASPYGSLRQHPPWAAPAHVPPPPQANWGWFAEPPGTSPEVAPDLA 728
Qy 130 ----- 129
Db 729 FVPRPFSRASRSRRRAAYCFPSPLIGSRRRRPHLSPQPSLSRLPQGGVTHSLPLGPLSP 788
Qy 130 ----- 129

```

Db 789 QLSLRGPPQPPPPRRRQSLREAFSLRRASGRGLGPPRSPVLGSPRPPSPPLLKHP 848
QY 130 -----PSKLPED-----DEPPAR-----PPPP----- 146
Db 849 RHRSNLPSRLPRTWRRLSEPTTRAVKPVWHRAYPPPPSAGPWGASTGALEQENQRRAE 908
QY 147 -----PPA----- 153
Db 909 DSETPTWVPLAPSMDVMDPPTQRPSPWPPEGISLGRSPPPVPENPLEHTSPSCPEP 968
QY 154 QAE----- 156
Db 969 QSEDRVSNLTGIFLGHQHDGPGQLTKSADPSLEKPEEVVTLGDRQPAEPALNPTPPN 1028
QY 157 -----PVM----- 159
Db 1029 KNVVSEKVLRLSASVPLVTCQARATWQWHRWKTVSRTAPLAPTRAPGPLLKAGEQP 1088
QY 160 -----TPPAPAPAPP----- 170
Db 1089 RAEPGRFAVMPQVRGVSSFRPKGPAPVQPPPEHPDQDPQGPAPQACSLRWFCLWPPTDA 1148
QY 171 -----STSV 174
Db 1149 HCLWSRIPTYSSQSHLRGHGGCHKSLMKKTRQSQWQNKQHSIRNLPMSRQHQREDGV 1208
QY 175 VLLLYWRDIIKTVGVFGASLFLLSLTVFSIVSVYATIALALLSVTISPRIYKGVIAIQ 234
Db 1209 EMTQLEDQETVL--ANL-----KTRFERNLIIYIYIGSILVSV----- 1246
QY 235 KSDEGHFRAYLESEVAISEELVQYSNSALG----- 266
Db 1247 -----NPYRMF-----AIYGEQVQVSGRALGPNPHLFAIANLAFKMLDAKQNCVVI 1297
QY 267 ----- 266
Db 1298 SGESGKTEATKLIRCLAMNQRDRVMQIKILEATPLEBAFGNAKTVRNDNSSRFK 1357
QY 267 -----HV----- 268
Db 1358 FVEIFLEGVICAITSYLLBKSRIVFOAKNERNYHIFYELLAGLPAQLROAFLQEA 1417
QY 269 -----NCTI-----KELRLIF----- 279
Db 1418 TYLYLNOGNCIEAGSDADDFFRLLAAMEVLGFTSEDQDSIFRILASILHLGNVVFEGH 1477
QY 280 -----LVD--D 283
Db 1478 ETDAQEVASVSGAREIQAVAELOVSPEGLQKAITFKVTETIREKIPTPLTVESAVDARD 1537
QY 284 LVDLSLKFAVLM-WVFYVGCAL-----FNLGLTLIL-----ALI 315
Db 1538 ATAKVLIALFWLITRVNALVSPKQDTLSIALDIYGFEDLSFNSPEQLCINYANENLQ 1597
QY 316 SLFSVPVVIYERHAQ----- 330
Db 1598 YLFN-KIVFOEQEVEIREQMDWEIAPADNQCINLISLKPYGILRLDDQCCFPQATD 1656
QY 331 -----IDHYLGLANKV-----KDM----- 346
Db 1657 HTFLQKCHYHGANPLYSKPMPLPEFTIKHYAGKVTYQVHKFLDKNHQVQVRQVLDLDFV 1716
QY 347 -----AKIQAKIPGLKRAE 361
Db 1717 HSRTRVVAHLFSSHAAQATAPPLRGKSSSITRLYKAHTVAAKTQOSLLDLVEKWE 1770

RESULT 14
T31065
diaphanous protein homolog p140mDia - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31065

R:Watanabe, N.; Madaule, P.; Reid, T.; Ishizaki, T.; Watanabe, G.; Kakizuka, A.; Saito, Y.
EMBO J. 16, 3044-3056, 1997
A:Title: p140mDia, a mammalian homolog of Drosophila diaphanous, is a target protein for
A:Reference number: Z20961; MUID:97357293; PMID:9214622
A:Accession: T31065
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1255 <WAT>
A:Cross-references: UNIPROT:O08808; EMBL:U96963; NID:G2114472; PID:G2114473; PIDN:AAC532E
A:Note: binds to GTP-bound form of Rho and binds to profilin

Query Match 13.9% Score 256.5; DB 2; Length 1255;
Best Local Similarity 14.7%; Pred. No. 3.9;
Matches 130; Conservative 42; Mismatches 135; Indels 575; Gaps 31;
QY 6 QSLVSSSDSPRPQ-----PAF----- 23
Db 406 QHLLVRNDYEARPOYKLIBECVSQIVLHKNGTDPDFKCRHLQIDIERLVDQMDTKTKV 465
QY 24 -----KYQFVREP 31
Db 466 EKSEAKATELEKCLDSELTARHELOVEMKMKNDPEQKLQDLQGEKDALDSEKQITAK 525
QY 32 EDEEE-----BEEDEDEDELELEVLERKPAAGLSAAPVPTAPAGAPLMDP 81
Db 526 QDLEAEVSKLTGEVAKLSKELEDKAKNEMASLAVVAVPSVSSAAVPPAPPLPG--DS 581
QY 82 GNDFVPPAPRGLPA-----APPVAP----- 102
Db 582 GTVIPPPPPPLPGVVPSPPLPGTCIPPPPLPGACIPPPPLPGSAAIPPPPL 641
QY 103 ---ERQPSWDSPSSSTVPAPSPISAAAASPSKLPEDDEPPARP----- 143
Db 642 PCVASIPPPPLPGATAIPPPPLPGATAIP-----PPPLPGTGIGIPPPPLPGSV 694
QY 144 ---PPPPASVSQAEVWTPPAPAPAP-----PSTSVV----- 175
Db 695 GVPPPPPLPGGGLPP---PPPPFGAPGIPPPPGMGVPPPPPPPPGFGVPAAPVLPFGLT 751
QY 176 -----DL---LYWRDIK----- 184
Db 752 PKVYKPEVQLRRPNWSKFVAEDLSQDCFWTVKEDRFENNELFAKLTLAFSAQTKSKA 811
QY 185 -----KT----- 186
Db 812 KKDQEGGEKSVQKKVKYKLVLDKTAQNLSIFLGSFRMPYQBIKKNVLEWNEAVLTE 871
QY 187 -----GVVFG-----ASLFLLSLT 201
Db 872 SMIQNLIKOMPEPEQKMLSELKEEYDDLAESQFGVVMGTVPRLRPRLNAILFKL---- 927
QY 202 VFS-----IVSVTA-----VIALALL-----SVTISF- 223
Db 928 QFSEQVENIKPEIVSVTAACEELRKSENFSLSLETLVGNVYNAGSRNAGAFGNISPL 987
QY 224 ---RIYKGVIAI-----OKSDEGHP-----FRAYLESEVAISELVOK----- 259
Db 988 CKLRDTKSADQCKTLLHFLAEICENDHPEVLKFPDELAAHVEKASRVSANLQSLDOMKK 1047
QY 260 -----YNSALGHVN---CTIKEL----- 275
Db 1048 QTADVERDVQNPAAATDEKDFEVRWTSFVKDAQEQYNKLRMMHSMNETLYKELGDFYVF 1107
QY 276 -----RRLFL----- 280
Db 1108 DPKLUSVEEFFMDLHNFNNFLOAVKENQKRETEKRRAKLAKEAKEKELEKQKKE 1167
QY 281 -----VDDLVDLSLKFAVLMWVFTYVGFALFNGLTLLILALISLFSVPVIVER 326
Db 1168 QLIDMNAEGDETVGMDLSLEALQ-----SCAAFR-----RKR 1199
QY 327 HQAQIDHYLG-----LANKVVK-DAMAKIQAKIPGLKRAE 361

Db	1200	GPQVNRKACAVTSLASELTDDAMAPGVKVP---KKSE 1238
RESULT 15		
A59266		
unconventional myosin-15 - human		
C:Species: Homo sapiens (man)		
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004		
C:Accession: A59266		
R:Liag, Y.; Wang, A.; Belyantseva, I.A.; Anderson, D.W.; Probst, F.J.; Barber, T.D.; Mian, T.B.; Fridelli, R.A.		
Genomics 61, 243-258, 1999		
A:Title: Characterization of the human and mouse unconventional myosin XV genes responsible for non-syndromic deafness		
A:Reference number: A59266; MUID:20021762; PMID:10552926		
A:Accession: A59266		
A:Status: preliminary; not compared with conceptual translation		
A:Molecule type: mRNA		
A:Residues: 1-3530 <LIA>		
A:Cross-references: UNIPROT:Q9UKN7; GB:AF144094; NID:g6224682; PIDN:AAF05903.1; PID:g6224682		
F:1225-1887/Domain: myosin motor domain homology <NMO>		
Query Match 13.8%; Score 255.5; DB 2; Length 3530;		
Best Local Similarity 9.9%; Pred. No. 57;		
Matches 140; Conservative 41; Mismatches 125; Indels 1105; Gaps 36;		
QY	16	PPRPQPAFKYF-----VREPEDEEEE-----EE-----41
Db	416	PTTPSPHNPYAHAMDDIAELEPEDEGVERQGTFRLPAAFFEQGMDKPARSKLSLR 475
QY	42	-----EEDEDELEL-----52
Db	476	KFLRPPRQVKLGKLEVLPPSLDPLPLGDADEEDELPPVSAVPYGHFWGFL 535
QY	53	-----EVLERKPAAGLS-----64
Db	536	TPQRNLQRALSAGAHGILGFGFGRVPRPATSILARFLKTKLSEKKPIARLGSQKT 595
QY	65	-----64
Db	596	RAGGAPVREAAKYRFGYKLAGMDPEKPGTPIVLRRAQPRARSSNDARRPPAPQAPRTLS 655
QY	65	-----AAP--VPTAPA 73
Db	656	HWSALLSPVPPRPPSSGPPAPPPLSGLPRPASPYGSLRRHPPPPWAAAPAHVPPAQ 715
QY	74	AG-----APLMD 80
Db	716	ASGWAFVEPPAVSVEVPPDLLAPPGRPSGRSRRGAAFGFGASPRASRRRAWSPLAS 775
QY	81	-----FGNDFVPPA-----89
Db	776	POPSSRLSSPGLGYCSPPLAPPSPQLSLRTGTFQFPFLPARRPRSLQESAPARRAAGRLGP 835
QY	90	-----PRGPLPAAPPV-----100
Db	836	PGSPLPGSRPPSPPLGLCHSPRRSSUNLPSRLPHTWRRLSEPPTRAVKPVQLRPLPHRPP 895
QY	101	-----APERQPSWD-----109
Db	896	RAGAWRAPLEHRSREPEDESETPTWTPPLAPSDVDMDPTQRPSPWPGGAGSRGRGFSR 955
QY	110	PSPVSTV-----PAPSP-----LSAAAVSPSK-----132
Db	956	PPVPVNPFLQLLGPVSPPTLPQEDPAADMTRVFLGRHHHPGPGQLTKGAGPTPEKPEEB 1015
QY	133	-----LPEDDEPPARPP-----145
Db	1016	ATLGDPLPAETKPTTAPPKVTPPKDITPPKDVLPQKTLRPSLSYPLAACDQTRATW 1075
QY	146	PP-----PASV 151
Db	1076	PPWHRWGTLPOAAAPLAPITRAPEPLPKGGRROAAGRFVAVMVRVQKLSSFORVGPATL 1135

QY	152	SQAEPVWTP-----PAP-----APAA-----168
Db	1136	KPQVQPIQDPKPRACSLRWSCLWLADAYCPWPRVHTHPQSCHLGPAAACLSLRGSWEV 1195
QY	169	-PPS-----TSVVDLLYMRDIKKTGVVFGASLPLLLSLTVFSI 205
Db	1196	GPSPWRNKMHSIRNLPSMRPREQHGEGVEDMTQLEDLOET-----TVLSN 1241
QY	206	VSVT-----AYIALALLSVT--ISFRIYKGVIAIQKSDGHPFRAYLESEVAISEEL 256
Db	1242	LKIRFERNLITYTVIGSILSVNPNYQMGIV-----GPEQ 1275
QY	257	VQKYSNSALG-----266
Db	1276	VOQYNGRAGLGNPPHPLFAVANLAFAMKLDKQNCIIISGSGSGKTEATKLIRLYAAM 1335
QY	267	-----266
Db	1336	NQKREVMQIKILEATPILLESFGNKTVRDNRSSRFKPVETFLGGVIGSAITSQYLLE 1395
QY	267	-----HV-----NCTI-----KEL 275
Db	1396	KSRIVFOAKNERNYHIFYELLAGLPAQLRQAFSLQEAETVYVYLNQGNCEIAGKSDADD 1455
QY	276	RRLF-----279
Db	1456	RLLAAMEVLGFSSEDDQSIFRILASILHLGNVYFEKYETDAQEASVVSAREIQVAEL 1515
QY	280	-----LVD--DLVDSLKFVLM-WVFTYVYCAL- 303
Db	1516	LQISPEGLQKAITFKVTETMREKIFPTPLTVESNVDARDAIAKLYIALLSWLTIRNALV 1575
QY	304	-----FNLTLIL-----ALISLFSVPVIYERHQ-----AQID- 332
Db	1576	SPQDRLSTAILDYGFEDLSFNSPEQLCINVANENLQVLFNKIVFOEEQEEVIREQIDW 1635
QY	333	-----332
Db	1636	QBITPADNQRINLISLKPYGILRLDDQCCFPQATDHTFLQKCHYHGHGANPLYSKPMP 1695
QY	333	-----HYLGLANKV-----KDM-----346
Db	1696	LPEFTIKHYAGKTYQVHKFELDKNHDQVQDVLDFVRSTRVVAHLFSSHAPQAAPQL 1755
QY	347	-----AKIQAKIPGLKRAE 361
Db	1756	GKSSSVTRLYKAHTVAAKFOQSILLIVERKE 1786

Search completed: June 23, 2005, 10:57:02
Job time : 33.0347 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2005, 10:17:56 ; Search time 114.158 Seconds
(without alignments)
1619.338 Million cell updates/sec

Title: US-09-830-972-29-FUSED

Perfect score: 1850

Sequence: 1 MEDLQSPVSSSDSPRPQ.....VKDAMAKIQKIPGLKRAE 361

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.1

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1933.9	99.1	392	2 Q96B16	Q96B16 homo sapien
2	1756.9	95.0	1192	1 RTN4 HUMAN	Q9ncq3 homo sapien
3	1669.8	90.3	343	2 Q6IPN0	Q6ipn0 homo sapien
4	1533	82.9	375	2 Q8BHF5	Q8bhf5 mus musculus
5	1523.1	82.3	356	2 Q8BH78	Q8bh78 mus musculus
6	1513	81.8	357	2 Q8K3G7	Q8k3g7 mus musculus
7	1478.8	79.9	1163	1 RTN4_RAT	Q9jkl1 rattus norv
8	1455.3	78.7	1162	2 Q8BGM9	Q8bgm9 mus musculus
9	1441.2	77.9	1163	2 Q8K3G8	Q8k3g8 mus musculus
10	1028	55.6	986	2 Q8IU44	Q8iu44 homo sapien
11	994	53.7	1046	2 Q8BCK7	Q8bck7 mus musculus
12	989.2	53.5	639	2 Q8K290	Q8k290 mus musculus
13	986.8	53.3	578	2 Q8QW95	Q8qw95 mus musculus
14	974.6	52.7	658	2 Q6R5S8	Q6rs58 gallus gall
15	927	50.1	199	2 Q7YRW9	Q7yrw9 bos taurus
16	923	49.9	199	2 Q6IM70	Q6im70 sus scrofa
17	919	49.7	187	2 Q6IG15	Q6igl15 sus scrofa
18	918	49.6	199	2 Q7PCJ7	Q7pcj7 macaca fasc
19	914.5	49.4	1024	2 Q6JRV2	Q6jrv2 xenopus lae
20	912.6	49.3	1043	2 Q6JRV0	Q6jrv0 xenopus lae
21	912.4	49.3	1055	2 Q6JRV1	Q6jrv1 xenopus lae
22	911	49.2	199	1 RTN4 MOUSE	Q99p72 mus musculus
23	903.8	48.9	315	2 Q6IF74	Q6if74 xenopus tro
24	900.5	48.7	330	2 Q6JRV4	Q6jrv4 xenopus lae
25	897.2	48.5	311	2 Q6JRV3	Q6jrv3 xenopus lae
26	886.4	47.9	1013	2 Q6JRV9	Q6jrv9 xenopus lae
27	884.5	47.8	1032	2 Q6JRV7	Q6jrv7 xenopus lae
28	883.3	47.7	1044	2 Q6JRV8	Q6jrv8 xenopus lae
29	883.2	47.7	199	2 Q7T224	Q7t224 gallus gall
30	881.2	47.6	323	2 Q6JRW1	Q6jrw1 xenopus lae
31	878.9	47.5	304	2 Q6JRW0	Q6jrw0 xenopus lae

32	873.1	47.2	316	2 Q6JRW2	Q6jrw2 xenopus lae
33	867	46.9	179	2 Q9GM33	Q9gm33 macaca fasc
34	829.8	44.9	780	2 Q8K0T0	Q8k0t0 mus musculus
35	827.7	44.7	776	1 RTN1_HUMAN	Q16799 homo sapien
36	825.8	44.6	780	2 Q8K4S4	Q8k4s4 mus musculus
37	818.1	44.2	777	1 RTN1_RAT	Q64548 rattus norv
38	793.3	42.9	760	2 Q90638	Q90638 gallus gall
39	793	42.9	193	2 Q6IF15	Q6if15 xenopus tro
40	781	42.2	193	2 Q6JRV6	Q6jrv6 xenopus lae
41	779.7	42.1	199	2 Q6PB23	Q6pb23 xenopus lae
42	752	40.6	193	2 Q6JRW4	Q6jrw4 xenopus lae
43	751.7	40.6	199	2 Q6JRW3	Q6jrw3 xenopus lae
44	750.9	40.6	214	2 Q7T222	Q7t222 carassius a
45	732	39.6	196	2 Q6IE16	Q6ie16 cyprinus ca

ALIGNMENTS

RESULT 1

Q96B16	PRELIMINARY;	PRT;	392 AA.
ID Q96B16;			
AC Q96B16;			
DT 01-DEC-2001 (TrEMBLrel. 19, Created)			
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)			
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)			
DE Reticulon 4, isoform D (RTN4 isoform B2).			
GN Name=RTN4;			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Kidney;			
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,			
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,			
RA Jones S.J., Marra M.A.;			
RT "Generation and initial analysis of more than 15,000 full-length human			
RT and mouse cDNA sequences."			
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN [2]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Kidney;			
RA Strausberg R.;			
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
RN [3]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;			
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;			
RT "Genomic structure and functional characterisation of the promoters of			
RT human and mouse nogorrt4."			
RL J. Mol. Biol. 325:299-323(2003).			
RN [4]			
RP SEQUENCE FROM N.A.			
RA Van der Putten H.;			
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.			
DR EMBL; BC016165; AAH16165.1; -.			

SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
MEDLINE=20237542; PubMed=10773680;
Yang J., Yu L., Bi A.D., Zhao S.-Y.;
"Assignment of the human reticulon 4 gene (RTN4) to chromosome 2p14--2p13 by radiation hybrid mapping.";
Cytogenet. Cell Genet. 88:101-102(2000).
[4]
SEQUENCE FROM N.A. (ISOFORM 4).
Jin W.-L., Ju G.;
"Developmentally-regulated alternative splicing in a novel Nogo-A.";
Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
[5]
SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
TISSUE=Placenta, and Skeletal muscle;
Ito T., Schwartz S.M.;
"Cloning of a member of the reticulon gene family in human.";
Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
[6]
SEQUENCE FROM N.A. (ISOFORM 2).
TISSUE=Fibroblast;
Yutsudo M.;
"Isolation of a cell death-inducing gene.";
Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
[7]
SEQUENCE FROM N.A. (ISOFORM 3).
TISSUE=Pituitary;
Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X., Luo B., Hu R., Chen J.;
"Human neuroendocrine-specific protein C (NSP) homolog gene.";
Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
[8]
SEQUENCE FROM N.A. (ISOFORM 3).
Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P., Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y., Yu J., Han L.H.;
"Novel human cDNA clones with function of inhibiting cancer cell growth.";
Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
[9]
SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE=Brain;
MEDLINE=99156230; PubMed=10048485;
Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirose M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
Mol. Cell Res. 5:355-364(1998).
[10]
SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
TISSUE=Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;
MEDLINE=2238257; PubMed=1477932; DOI=10.1073/pnas.242603899;
Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smolius D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[11]


```
DR EMBL; AY102282; AAM73504.1; -.
DR EMBL; AY102286; AAM73509.1; -.
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:000515; F:protein binding; IPI.
DR GO; GO:0005125; P:angiogenesis; IMP.
DR GO; GO:0007399; P:neurogenesis; IDA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 375 AA; 40300 MW; 23D9EB19BB671AE6 CRC64;

Query Match      82.9%; Score 1533; DB 2; Length 375;
Best Local Similarity 82.8%; Pred. No. 7.4e-42;
Matches 317; Conservative 13; Mismatches 23; Indels 30; Gaps 7;

QY 1 MEDLQSPVLVSS--DSPRRPQPAFKYQVREPEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDELEVLKRP 59
Db 1 MEDIDQSSLVSSADSPRRPQPAFKYQVTEPEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDELEVLKRP 60
QY 60 AAGLSAAPTAPAGAPLMDFGNDFVPAPRGPLPAAPVAPRQPSWDPSVSTVPA 119
Db 61 AAGLSAAPTAP--PAA-APLDFSSDVPAPRGPLPAAPTAPRQPSWERSPAAS---A 114
QY 120 PSLPLSAAVPSKLPEDDEPPAPPPPPASVSPQAEPTWTPAPA----- 165
Db 115 PSLPAAAALVPSKLPEDDEPPAR--PPAPAGASPLAEPAAPSTPAAPKRRGSGVDETL 172
QY 166 ---PAAP-----PSTSVLDLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTVAYIALALLS 218
Db 173 PALPASEPVISSAVVLDLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTVAYIALALLS 232
QY 219 VTISPRIYKGVIAQIKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCITIKELRL 278
Db 233 VTISPRIYKGVIAQIKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCITIKELRL 292
QY 279 FLVDDLDVLSKFAVLMMWFTYVGFALFNGTLILALISLFSVPVIYERHQAQIDHYLGIA 338
Db 293 FLVDDLDVLSKFAVLMMWFTYVGFALFNGTLILALISLFSVPVIYERHQAQIDHYLGIA 352
QY 339 NKNVKDAMAKIQAKIPGLKRAE 361
Db 353 NKSVDAMAKIQAKIPGLKRAE 375

RESULT 5
ID QBH78 PRELIMINARY; PRT; 356 AA.
AC QBH78;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE RTN4.
GN Name=Rtn4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVCJ7; and 129SVCJ7;
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT "Genomic structure and functional characterisation of the promoters of
human and mouse nogo/rtn4."
RL J. Mol. Biol. 325:299-323(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVCJ7;
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.

RC STRAIN=129SVCJ7;
RA Van der Putten H., Mir A.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102286; AAM73503.1; -.
DR EMBL; AY102286; AAM73508.1; -.
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:000515; F:protein binding; IPI.
DR GO; GO:0005125; P:angiogenesis; IMP.
DR GO; GO:0007399; P:neurogenesis; IDA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 356 AA; 38403 MW; 4366C03BA9630B56 CRC64;

Query Match      82.3%; Score 1523.1; DB 2; Length 356;
Best Local Similarity 84.5%; Pred. No. 1.4e-41;
Matches 315; Conservative 11; Mismatches 18; Indels 29; Gaps 7;

QY 1 MEDLQSPVLVSS--DSPRRPQPAFKYQVREPEDEDEDEDEDEDEDEDEDEDEDEDELEVLKRP 59
Db 1 MEDIDQSSLVSSADSPRRPQPAFKYQVTEPEDEDEDEDEDEDEDEDEDEDEDELEVLKRP 60
QY 60 AAGLSAAPTAPAGAPLMDFGNDFVPAPRGPLPAAPVAPRQPSWDPSVSTVPA 119
Db 61 AAGLSAAPTAP--PAA-APLDFSSDVPAPRGPLPAAPTAPRQPSWERSPAAS---A 114
QY 120 PSLPLSAAVPSKLPEDDEPPAPPPPPASVSPQAEPTWTPAPA----- 173
Db 115 PSLPAAAALVPSKLPEDDEPPAR--PPAPAGASPLAE-----PAAPSTPAAPKRR 163
QY 174 -----VDLLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTVAYIALALLSVTSPIYK 228
Db 164 GSGSVVLDLYWRDIKKTGVFGASLFLLLSLTVFSIVSVTVAYIALALLSVTSPIYK 223
QY 229 VIQATQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCITIKELRLFLVDDLDVLS 288
Db 224 VIQATQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCITIKELRLFLVDDLDVLS 283
QY 289 KFAVLMMWFTYVGFALFNGTLILALISLFSVPVIYERHQAQIDHYLGIANKNVKDAMAK 348
Db 284 KFAVLMMWFTYVGFALFNGTLILALISLFSVPVIYERHQAQIDHYLGIANKNVKDAMAK 343
QY 349 IQAKIPGLKRAE 361
Db 344 IQAKIPGLKRAE 356

RESULT 6
ID QBK3G7 PRELIMINARY; PRT; 357 AA.
AC QBK3G7;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Nogo-B.
GN Name=Rtn4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Jin W., Li R., Long M., Shen J., Ju G.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY114153; AAM77069.1; -.
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 357 AA; 38566 MW; 73BB3D17DFDBDF15 CRC64;
```



```
FT CONFLICT 1130 1131 Missing (in Ref. 3: AAD31020).
SQ SEQUENCE 1163 AA; 126386 MW; 8CB894B09E94F086 CRC64;

Query Match
Best Local Similarity 27.4%; Pred. No. 6.1e-39;
Matches 320; Conservative 11; Mismatches 25; Indels 812; Gaps 7;

QY 1 MEDLOSPLVSSS-DSPRPQPAFKYQFVREDEDER-EEEEEEEEDEDDLELEVLK 58
DB 1 MEDIQSSILVSSSTSPRPFPFAFKYQFVTEPEDEDEDEDEDEDDLELEVLK 60

QY 59 PAAGLSAAVPPTAPAGALMDFGNDVPAPRGPLPAAAPPVAPRQPSWDPSPVSTVP 118
DB 61 PAAGLSAAVP--PAAALPDLFSSDVPAPRGPLPAAAPPVAPRQPSWERSPAA---P 115

QY 119 APSPLSAAAVSPKLPEDDEPPARPPPPASVSPQAEFVWTPPAPA----- 165
DB 116 AFSPLPAAAVLSPKLPEDDEPPARPPPPAGASPLAEPAPSTPAAPKRRGSGVDST 175

QY 166 ----PAA----- 168
DB 176 LPALPAASEPVPISSAEKIMDLMEQPGNTVSSGQEDFPSSVLLETAASPLSPLSTVSPK 235

QY 169 ----- 168
DB 236 EHYGLNLAVSSSEGTIBETLNEASKELPERATNPVNRDLAEPSELSEYSEMGSSFKGS 295

QY 169 ----- 168
DB 296 PKGESAILVENTKEEVIVRSKEDLVCSAALHSPOESPVGKEDRVSPKTDIFNEMQ 355

QY 169 ----- 168
DB 356 MSVAPVRBEYADFKPFEQAWKDYEGSRDVLAAARANVESKVDKCLEDSLEQKSLGK 415

QY 169 ----- 168
DB 416 DSEGRNEDASPTPEPVKDSRAYITCASFTSATESSTANTPPLLEDHTSENKTKDEKI 475

QY 169 ----- 168
DB 476 BERKAQIITEKTSPTKSNPLVAVQDSADYVTTDLTSKVTEAANVMPEGLTPDLVQEA 535

QY 169 ----- 168
DB 536 CESELNEATGTKIAYETKVDLVQTSBAIQESLYPTAQLCPSPPEAEATPSVLPDIMEA 595

QY 169 ----- 170
DB 596 PLNSLLPSAGASVQPSVSPLEAPPVSYDSIKLEPENPPPYEEAMNVALKALGKKGK 655

QY 171 ----- 170
DB 656 EPESFNAAVQTEAPYISTACDLIKETKLTSPSPDPSNYSIAKFEKSPHEAELVEDS 715

QY 171 ----- 170
DB 716 SPESEPVDLFSDSISPEVPQTQBEAVMLMKSLTEVSETVAQHKBERLSASQELGKPYL 775

QY 171 ----- 170
DB 776 ESFQPNLHSTKDAASNDIPTLTKEKIKSLQMEEFNTAIYSNDLISKEDKIKESSETFSD 835

QY 171 ----- 170
DB 836 SSPIETIDEPPTFVSAKDSPLKAEYTDLEVDSKSEIANIOSGADSLPCLELPCLDSFK 895

QY 171 ----- 170
DB 896 NIYPKDEVHSDSEFSENRSVSKASISPSNVALEPQTEMGSIKSVSKSLTKEAKKLPSD 955

QY 171 -----STSVDDLWDRDKTKTGVVFGASLFLLSLTVFSIVSVTAYTA 213
DB 171 -----STSVDDLWDRDKTKTGVVFGASLFLLSLTVFSIVSVTAYTA 213
```

```
DB 956 TEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYTA 1015
QY 214 LALLSVTTSFRIYKGVIAIQKSDGHPFRAYLSEVAISELQKYSNSALGHVNCNTIK 273
DB 1016 LALLSVTTSFRIYKGVIAIQKSDGHPFRAYLSEVAISELQKYSNSALGHVNCNTIK 1075
QY 274 ELRRFLVDDLVDSLKFAVLMVFTYVVGALFNGLTLLILALISLSPVPIYERHQAIQIDH 333
DB 1076 ELRRFLVDDLVDSLKFAVLMVFTYVVGALFNGLTLLILALISLSPVPIYERHQAIQIDH 1135
QY 334 YLGLANKVVKDAMAKIQAKIPGLKKAKE 361
DB 1136 YLGLANKVVKDAMAKIQAKIPGLKKAKE 1163

RESULT 8
Q8BGM9 PRELIMINARY; PRT; 1162 AA.
AC Q8BGM9;
DT 01-MAR-2003 (TREMELrel. 23, Created).
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE RTN4.
GN Name=RTN4;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7; and 129SVCJ7;
RX MEDLINE=22376340; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT "Genomic structure and functional characterisation of the promoters of
RT human and mouse nogo/rtn4.";
RL J. Mol. Biol. 325:299-323(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7;
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129SVCJ7;
RA Van der Putten H., Mir A.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY102284; AAM73506.1; -
DR EMBL; AY102286; AAM73511.1; -
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0001525; P:angiogenesis; IMP.
DR GO; GO:0007399; P:neurogenesis; IDA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 1162 AA; 126612 MW; 855697PBEE11781F CRC64;

Query Match
Best Local Similarity 78.7%; Score 1455.3; DB 2; Length 1162;
Matches 319; Conservative 11; Mismatches 23; Indels 817; Gaps 8;

QY 1 MEDLOSPLVSSS-DSPRPQPAFKYQFVREPEDEDEDEDEDEDEDEDEDEDELELEVLK 59
DB 1 MEDIQSSILVSSADSPRPFPFAFKYQFVTEPEDEDEDEDEDEDEDEDEDEDELELEVLK 60

QY 60 AAGLSAAVPPTAPAGALMDFGNDVPAPRGPLPAAAPPVAPRQPSWDPSPVSTVPA 119
DB 61 AAGLSAAVP--PAA-APLDFSSDVPAPRGPLPAAAPPVAPRQPSWERSPAA---A 114

QY 120 PSPLSAAVSPKLPEDDEPPARPPPPASVSPQAEFVWTPPAPA----- 165
DB 115 PSPLSAAVSPKLPEDDEPPAR--PPAPAGASPLAEPAPSTPAAPKRRGSGVDL 172
```

```
QY 166 ---PAA----- 168
DB 173 FALPAASEPVIPSSAEKIMDLKEQPGNTVSSGQEDFPSPVLPTAASLPSLSPLSTVSPKE 232
QY 169 ----- 168
DB 233 HGYLGNLSAVASTECTIBETLNEASRELPERATNPFVNRESAEFVLEYSMSGSSFNQSP 292
QY 169 ----- 168
DB 293 KGESAMLVENTKEEVIVRSKDKEDLVCSAALHNPOESPATLTQVVKEDGVMSPEKTMDF 352
QY 169 ----- 168
DB 353 NEMKMSVAVPVREEYADPKPEQAEVKTDEGSRDVLAAANMESKVDKCKCFEDSLQK 412
QY 169 ----- 168
DB 413 GHGKDESRNENASFPPTPELVKDGSRAYITCDSFSSATESAANI FVLEDTSENKTD 472
QY 169 ----- 168
DB 473 EKKIERKAQIITEKTSKPTSNPFLVAIHDSEADYVTTDNLSKVTEAVVATMPEGLTDPDL 532
QY 169 ----- 168
DB 533 VQACESELNEATGKIAETKVDLVQTSSEIYPTAQICPSFBEAEATPSVLPDI 592
QY 169 ----- 170
DB 593 VMEAPLNSLLPSTGASVAQPSASPLEVSPVSDGKLEPENPPPYEAMSVALKTSDAK 652
QY 171 ----- 170
DB 653 BEIKPEPESFNAQAEAPYISACDLIKETKLTSTEPSPEFSNYSEIAKFKSVDPHCEL 712
QY 171 ----- 170
DB 713 VDDSSPEPDLFSDSDSIPEVPQTEAEVLMKESLTVSTVTHKHKRLSASPOEV 772
QY 171 ----- 170
DB 773 GRPYLESFQPNLHTKDAASNEIPTLTKEITISLQWBEFNTAIYSDNDLLSKDKMKES 832
QY 171 ----- 170
DB 833 ETFSDSPTEIIDEPTTFVSAKDSKPEYTDLEVNKSEIANVQSGANSLPCSELPCDLS 892
QY 171 ----- 170
DB 893 FKNTYKDEAHVSDFSKSRSSVKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEKLP 952
QY 171 -----STSVDDLWYRDITKKTGVFGASLFLLLSLTVPSIVSVTAY 211
DB 953 SDTEKEDRSALTAVLSAELNKTSDWLLYWRDITKKTGVFGASLFLLLSLTVPSIVSVTAY 1012
QY 212 IALALLSVTISPRIYKGVITQAKDEGHPFRAYLESEVAISEELVQKYSNLSALGHVNST 271
DB 1013 IALALLSVTISPRIYKGVITQAKDEGHPFRAYLESEVAISEELVQKYSNLSALGHVNST 1072
QY 272 IKELRRLFLVDDLVSALFAVLMWFTYVVGALFNGLTLLILALISLFSVPVYRHRQAI 331
DB 1073 IKELRRLFLVDDLVSALFAVLMWFTYVVGALFNGLTLLILALISLFSVPVYRHRQAI 1132
QY 332 DHYLGANKNVKDAKQAKIPGLKRAE 361
DB 1133 DHYLGANKNVKDAKQAKIPGLKRAE 1162
```

RESULT 9

Q8K3G8

ID Q8K3G8

PRELIMINARY;

PRT; 1163 AA.

```
AC Q8K3G8;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Nogo-A.
GN Name=Rtn4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY114152; AAM77068.1; -.
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:cytoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 1163 AA; 126690 MW; 6B5F362799417EA4 CRC64;
```

Query Match 77.9%; Score 1441.2; DB 2; Length 1163;

Best Local Similarity 27.2%; Pred. No. 1e-37;

Matches 318; Conservative 11; Mismatches 24; Indels 818; Gaps 9;

QY 1 MEDDQSLVSS--DPPRPOPAKYQVREPEDEEEEEDEDEDEDEDELEVLKRP 59

DB 1 MEDDQSLVSSADSPRPAPKQYVTPDEDEDEDEDEDEDEDEDELEVLKRP 60

QY 60 AAGLSAAPVTPAAGAPLMDFGNDVPPAPRGLPAPPVAPRQPSWDPSPVSTVPA 119

DB 61 AAGLSAATVPP--PAA-APLDFSSDVPAPRGLPAPPTAPRQPSWSPASPAAS--A 114

QY 120 PSLPSAAVSPSKLPEDDEPPAPRPPPPASVQAEVPTTPAPA----- 165

DB 115 PSLPAAAALVPSKLPEDDEPPAR--PPAPAGASPLAEPAAPSTPAAPKRKSGSVDEL 172

QY 166 ---PAA----- 168

DB 173 FALPAASEPVIPSSAEKIMDLKEQPGNTVSSGQEDFPSPVLPTAASLPSLSPLSTVSPKE 232

QY 169 ----- 168

DB 233 HGYLGNLSAVASTECTIBETLNEASRELPERATNPFVNRESAEFVLEYSMSGSSFNQSP 292

QY 169 ----- 168

DB 293 KGESAMLVENTKEEVIVRSKDKEDLVCSAALHNPOESPATLTQVVKEDGVMSPEKTMDF 352

QY 169 ----- 168

DB 353 NEMKMSVAVPVREEYADPKPEQAEVKTDEGSRDVLAAANMESKVDKCKCFEDSLQK 412

QY 169 ----- 168

DB 413 GHGKDESRNENASFPPTPELVKDGSRAYITCDSFSSATESAANI FVLEDTSENKTD 472

QY 169 ----- 168

DB 473 EKKIERKAQIITEKTSKPTSNPFLVAIHDSEADYVTTDNLSKVTEAVVATMPEGLTDPDL 532

QY 169 ----- 168

DB 533 VQACESELNEATGKIAETKVDLVQTSSEIYPTAQICPSFBEAEATPSVLPDI 592

QY 169 ----- 170

DB 593 VMEAPLNSLLPSTGASVAQPSASPLEVSPVSDGKLEPENPPPYEAMSVALKTSDAK 652

QY 171 ----- 170

Db 653 EEIKPESFNAAQAEAPYISACDLIKETKLSSTEPSPGFSNYSEIAKFEKSVDPHCEL 712
 QY 171 -----
 Db 713 VDDSSPESEPVDLFSDSDSIPEVPOQEAAVLMKESLSEVSETVQHKHKLRSASPQEV 772
 QY 171 -----
 Db 773 GKPYLESPQNLHITKDAASNEIPTLTKKETISLQWEEFNATYISNDLLSSKEDMKES 832
 QY 171 -----
 Db 833 ETFSDSPIETIIDERTFTFVSAXDDSPKEYTDLEVSNKSEIANVQSGANSLPCSELPCLDS 892
 QY 171 -----
 Db 893 FRNTYPKDEAHVSDBFSSRSVSKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEKLP 952
 QY 171 -----
 Db 953 SSTEKEDSLTAVLSAELNKTSSVDLLYWRDIKKTGVYFGASLFLLSLTIVFSIVSVA 1012
 QY 211 YIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNC 270
 Db 1013 YIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNS 1072
 QY 271 TIKELRRLFLVDLVDLSLKFVLMVFTYVVGALFNLGLTLLIALLSLFSVPVIERHOAQ 330
 Db 1073 TIKELRRLFLVDLVDLSLKFVLMVFTYVVGALFNLGLTLLIALLSLFSVPVIERHOAQ 1132
 QY 331 IDHYLGLANKNVKDAWAKIQKIPGLKRAE 361
 Db 1133 IDHYLGLANKNVKDAWAKIQKIPGLKRAE 1163

RESULT 10
 Q8IUUA4 PRELIMINARY; PRT; 986 AA.
 AC Q8IUUA4;
 DT 01-MAR-2003 (TREMELrel. 23, Created)
 DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
 DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
 DE RNT4 (RTN4 isoform Ab) (RTN4 isoform D) (RTN4 isoform E) (RTN4 isoform F) (RTN4 isoform G) (RTN4 isoform Aa).
 GN Name=RTN4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
 RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
 RT "Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4.";
 RL J. Mol. Biol. 325:299-323 (2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Van der Putten H.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Oertle T., Schwab M.E.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY102285; AAM64244.1; -
 DR EMBL; AY123246; AAM64250.1; -
 DR EMBL; AY123247; AAM64251.1; -
 DR EMBL; AY123248; AAM64252.1; -
 DR EMBL; AY123249; AAM64253.1; -
 DR EMBL; AY123250; AAM64254.1; -

DR EMBL; AY123245; AAM64249.1; -
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS0845; RETICULON; 1.
 SQ SEQUENCE 986 AA; 108449 MW; 0CDE8F647036415A CRC64;
 Query Match 55.6%; Score 1028; DB 2; Length 986;
 Best Local Similarity 39.2%; Pred. No. 1.8e-24;
 Matches 250; Conservative 27; Mismatches 60; Indels 300; Gaps 17;
 QY 3 DLQDS-----PLVSSSDSPRRP-----Op--- 21
 Db 372 DLVQTSVWQSLYPAAQLCFSESEATPSPVLPIVMEAPLNSAVSAGASVITQSSS 431
 QY 22 -----AFKIQFVR-EPED-----EEEEEDEDEDELE 53
 Db 432 PLEASSVNYESIKHEPENPPPEEAMSVLKKVSGIKEEIKPENINAALQTEAPYISI 491
 QY 54 -----VLERKPAAGLSAAPV-----TAPAAGAPLMDFGNDP 85
 Db 492 ACDLIKETK-----LSAEPAPDFSDYSEMAKVQPVDPHSELVEDSSPOS-EPVDLFSDDS 546
 QY 86 VPPAP-----RGPLPAAP----- 99
 Db 547 IPDVQKQDQETVLMVKESLTETSPESMIEYENKEKLSALPPGKPYLESFKLSLDNTKD 606
 QY 100 -VAP-----ERQPSWDPSV----- 113
 Db 607 TLLPDEVSTLSKKEKIPLOMEELSTAVYVNDLFIKSAQIRETETFTSDSPIEIDEPF 666
 QY 114 ----- 113
 Db 667 TLISSTDSFSKLAREYTDLEVSHKSEIANAPDAGSLPCTELPHDLSLKNTQPKVEEKI 726
 QY 114 -----SSTVPAPSPLSAAA-----VSP-----SKLPEDDEPPARP 144
 Db 727 SFSDDFSKNGSATSKVLLLPDVSALATQAEIESIVKPKLVKEAEKKLPSTEKEDR-- 784
 QY 145 PPPASVSPQAEPPVWTPPAPAPAPSTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFS 204
 Db 785 -----SPSAIFSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFS 829
 QY 205 IVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNSA 264
 Db 830 IVSVTAYIALALLSVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISEELVQKYSNSA 889
 QY 265 LGHVNCTIKELRRLFLVDLVDLSLKFVLMVFTYVVGALFNLGLTLLIALLSLFSVPVIY 324
 Db 890 LGHVNCTIKELRRLFLVDLVDLSLKFVLMVFTYVVGALFNLGLTLLIALLSLFSVPVIY 949
 QY 325 ERHQAQIDHYLGLANKNVKDAWAKIQKIPGLKRAE 361
 Db 950 ERHQAQIDHYLGLANKNVKDAWAKIQKIPGLKRAE 986
 RESULT 11
 Q8BGK7 PRELIMINARY; PRT; 1046 AA.
 AC Q8BGK7;
 DT 01-MAR-2003 (TREMELrel. 23, Created)
 DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
 DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
 DE RTN4.
 GN Name=Rtn4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7; and 129SvCJ7;
 RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;

RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
 RT "Genomic structure and functional characterisation of the promoters of
 RT human and mouse nogo/rtn4";
 RL J. Mol. Biol. 325:299-323(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129SvCJ7;
 RC STRAIN=129SvCJ7;
 RA Van der Putten H.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129SvCJ7;
 RA Van der Putten H., Mir A.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY102280; AAM73502.1; -;
 DR EMBL; AY102286; AAM73507.1; -;
 DR MGD; MGI:1915835; Rtn4.
 DR GO; GO:0005783; C:Endoplasmic reticulum; IDA.
 DR GO; GO:0005515; P:protein binding; IPI.
 DR GO; GO:0001525; P:angiogenesis; IMP.
 DR GO; GO:0007399; P:neurogenesis; IDA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 1046 AA; 114221 MW; 8CE2E2238ED51222 CRC64;
 Query Match 53.7%; Score 994; DB 2; Length 1046;
 Best Local Similarity 38.6%; Pred. No. 2.6e-23;
 Matches 240; Conservative 31; Mismatches 73; Indels 278; Gaps 15;
 QY 3 DLQDS-----PLVSSSDSPPRP-----QPA-- 22
 Db 440 DLVQTSEAIQESIVPTAQLCPSEAEATPSPVLPIVMEAPLNSLLPSTGASVAQPSAS
 QY 23 -----FKYQFVR-EPDEDEEEEEE-----HEDEDEDELE 53
 Db 500 PLEVSPSPSYDGIKLEPENPPPYEEAMSVALKTSKKEIKPEPSFNAAAEAPYISI 559
 QY 54 -----VLERKPAAGLSAAPVP-----TAPAAGAPLMDFGNDF 85
 Db 560 ACDDLKETK-----LSTEPSPEFSNYSEIAKPEKSVDPHCELVDSSPES-EPVDFLSDS 614
 QY 86 VPPAPR-----GFLPAAPPVAPERQPSW----- 108
 Db 615 IPEVQTQEEAVMLKESITVETVTOHKHKERLSASPOEVGKPYLESFQNLHITKDA 674
 QY 109 -----DFSPVSVTPAPSP 122
 Db 675 ASNEIPTLTKEETISLOWMEEFNTAYSNDLLSSKEDKMKESITPFSDSPIEIIDFPTF 734
 QY 123 LSAAAVSP-----SKLPED-----DEPPARPPPPP 147
 Db 735 VSAKDDSPKEYTDLVSNKSEANTVQSGANSLPSELFCDSLFSKNTYKDE----- 785
 QY 148 PASVSPQAPVWTPPAPAPAPS----- 171
 Db 786 -AHVSDFSKSSRSVSKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEKLPSTDEKDR 844
 QY 172 -----TSVVDLLYWRDIKKTGVVFGASFLPILLSLVTSVTSVYALALLSV 219
 Db 845 SLTAVLSAELNKTSTVVDLLYWRDIKKTGVVFGASFLPILLSLVTSVTSVYALALLSV 904
 QY 220 TISPRIYKGVIOAKQSDGHPFRAYLESEVAISELVQKYSNLSALGHVNCITKELRLF 279
 Db 905 TISPRIYKGVIOAKQSDGHPFRAYLESEVAISELVQKYSNLSALGHVNCITKELRLF 964
 QY 280 LVDDLVDLSLKFVLMWFTYVVGALFNGLTLILALISLFSVPVIYERHQAQIDHYLGLAN 339
 Db 965 LVDDLVDLSLKFVLMWFTYVVGALFNGLTLILALISLFSVPVIYERHQAQIDHYLGLAN 1024
 QY 340 KVKDAMAKIQAKIGLKKRAE 361
 Db 1025 KSVKDMAMAKIQAKIGLKKRAE 1046

RESULT 12
 Q8K290 PRELIMINARY; PRT; 639 AA.
 ID Q8K290
 AC Q8K290;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Rtn4 protein.
 GN Name=Rtn4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC032192; AAH32192.1; -;
 DR MGD; MGI:1915835; Rtn4
 DR GO; GO:0005783; C:Endoplasmic reticulum; IEA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 639 AA; 70312 MW; 309A19DA37603F11 CRC64;
 Query Match 53.5%; Score 989.2; DB 2; Length 639;
 Best Local Similarity 38.6%; Pred. No. 1.2e-23;
 Matches 240; Conservative 31; Mismatches 73; Indels 278; Gaps 15;
 QY 3 DLQDS-----PLVSSSDSPPRP-----QPA-- 22
 Db 33 DLVQTSEAIQESIVPTAQLCPSEAEATPSPVLPIVMEAPLNSLLPSTGASVAQPSAS 92
 QY 23 -----FKYQFVR-EPDEDEEEEEE-----HEDEDEDELE 53
 Db 93 PLEVSPSPSYDGIKLEPENPPPYEEAMSVALKTSKKEIKPEPSFNAAAEAPYISI 152
 QY 54 -----VLERKPAAGLSAAPVP-----TAPAAGAPLMDFGNDF 85
 Db 153 ACDDLKETK-----LSTEPSPEFSNYSEIAKPEKSVDPHCELVDSSPES-EPVDFLSDS 207
 QY 86 VPPAPR-----GFLPAAPPVAPERQPSW----- 108
 Db 208 IPEVQTQEEAVMLKESITVETVTOHKHKERLSASPOEVGKPYLESFQNLHITKDA 267
 QY 109 -----DFSPVSVTPAPSP 122

Db 268 ASNEIPTLTKETISLOMEFNTAIYNSDDLLSSKEDKMKSETPSDSSPIEIIIDFFPTF 327
QY 123 LGAAYASP-----SKLPED-----DEPPARPPPP 147
Db 328 VSAKDDSPREYTDLEVSNKSEIANVQSGANSLPCSELPCDLSFKNTYPKDE----- 378
QY 148 PASVSPQAEFVTPPPAPAPAPS----- 171
Db 379 -AHVDEFKSSSSSVSKVLLLPNVSALESQIEMGNIVPKVLTKEAEKLPDTEKEDR 437
QY 172 -----TSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSTVSTAYIALALLSV 219
Db 438 SLTAVLSAELNKTSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSTVSTAYIALALLSV 497
QY 220 TISFRIYKGVIOAIQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRLRF 279
Db 498 TISFRIYKGVIOAIQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELRLRF 557
QY 280 LVDDLVDLSLKFAVLMMVFTYVGCALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLAN 339
Db 558 LVDDLVDLSLKFAVLMMVFTYVGCALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLAN 617
QY 340 KNVKDMAMAKIQKIPGLKKAEE 361
Db 618 KSVKDMAMAKIQKIPGLKKAEE 639

RESULT 13
Q80W95
ID Q80W95 PRELIMINARY; PRT; 578 AA.
AC Q80W95
DT 01-JUN-2003 (TremBLrel. 24, Created)
DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Nogo-A (Fragment).
GN Name=Nogo-A;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tozaki H., Hirata T.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073672; BAC75974.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
FT NON_TER 1
SQ SEQUENCE 578 AA; 63696 MW; 832670C171E4AC61 CRC64;

Query Match 53.3%; Score 986.8; DB 2; Length 578;
Best Local Similarity 41.1%; Pred. No. 1.1e-23;
Matches 232; Conservative 21; Mismatches 85; Indels 227; Gaps 8;

QY 7 SPLVSSD-----SPRPQAFKYQVREPDEEEEEDEDEDEDELELV----- 54
Db 31 SPLEVPSPVSDIGIKLEPNPPYEAMSVALKTSDAKEIKEPSPFNAQAQEAAPYIS 90
QY 55 -----LERKPAAGLS-----AAP-----VPTAPAGAPLMDFGNDFVPPA 89
Db 91 IACDLIKETKLTSPSPGFSNYSIAKPKSVDPHCELVDSSPSEPVDFLSDSDSIPEV 150
QY 90 PR-----GLPAPAPPVAPERQSW----- 108
Db 151 POTQEAANMKESTLEVSETVQHKHKLRSASQEVGKPYLESFQPNLHITKDAAGNE 210
QY 109 -----DPGPVSVSTVPAPPLSAA 126
Db 211 IPTLTKETISLOMEFNTAIYNSDDLLSSKEDKMKSETPSDSSPIEIIIDFFPTFVSAK 270

QY 127 AVSP----- 130
Db 271 DDSPEYTDLEVSNKSEIANVQSGANSLPCSELPCDLSFKNTYPKDEAHVDEFKSSRS 330
QY 131 -----SKLPEDDEPPARPPPPPPASVSPQAE 156
Db 331 VFVKVPLLLPNVSALESQIEMGNIVPKVLTKEAEKLPDTEKEDR----- 376
QY 157 PWMTPPAPAPAAPSTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSTVSTAYIALAL 216
Db 377 ---SLTAVLSAELNKTSSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSTVSTAYIALAL 433
QY 217 LSVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELR 276
Db 434 LSVTISFRIYKGVIOAIQKSDGHPFRAYLESEVAISELVQKYSNSALGHVNCITIKELR 493
QY 277 RULFLVDLVDLSLKFAVLMMVFTYVGCALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGL 336
Db 494 RULFLVDLVDLSLKFAVLMMVFTYVGCALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGL 553
QY 337 LANKNVKDMAMAKIQKIPGLKKAEE 361
Db 554 LANKNVKDMAMAKIQKIPGLKKAEE 578

RESULT 14

Q6RSS8

ID Q6RSS8 PRELIMINARY; PRT; 658 AA.
AC Q6RSS8
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Neurite outgrowth inhibitor NOGO-A (Fragment).
GN Name=NOGO;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Calharp S.A. Pira C.U., McNeill D.S., Liwnicz B.H., Oberg K.C.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY494005; AAS18427.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
FT NON_TER 1
SQ SEQUENCE 658 AA; 72075 MW; 14B7A000C5E8CDA5 CRC64;

Query Match 52.7%; Score 974.6; DB 2; Length 658;
Best Local Similarity 38.2%; Pred. No. 3.8e-23;
Matches 229; Conservative 32; Mismatches 84; Indels 254; Gaps 12;

QY 6 QSPLV-----SSDSPRPQAFKYQVREPDE 34
Db 71 EAPLSSGTAGAEASTVQLETSQGTFTVTASVENKKEAKPPYQEAVMPLTQAEAK 130
QY 35 EE-----EEEEDEDEDELE-----ELEVLERKPAAGLSAAP----- 67
Db 131 EELTLKADRESSTSPEDLETPTYSIACDLIKETKVSGESASPSLTDYSTTPTITEHLSQD 190
QY 68 -----VP 69
Db 191 VSEHKELAEKLSPOFGKCDLPSRQVMPDPGKESDQTLILNGKSVENIETDEEQLVD 250
QY 70 TAPAGAPLMDFGND-----FVPPAPRGPLPAPAPPVAPERQ----- 106
Db 251 SLAATGKPYLESFQDLSDSSKIVTTPQSEPTPAKIAKA-EKIPLQMEELNALAYSTDVSV 309
QY 107 SWDPSVSVSTVPAPPLSAAVSPSKLPED----- 136

Job time : 119.158 secs

Db 310 AMEPKPGDSKGLSPS-----SPVSVEDDFVMLVDPKGTGTEFVAEVTDRVTHKNESKD 362
 QY 137 -----DEPPARPPPPASVS-----POAEPVWTPAP 164
 Db 363 ISNEIRDEKROAPLTFLCDLSVRNVVEKTEDDAHALKKSLOAIDREVPEVSMV---SLP 419
 QY 165 APAAPP-----TSVVDLLYWRD 182
 Db 420 ATGTSPSTKEKIVSGKPEAKEAERGAASAKEKEKPTAVFSAKLVSSVVDLLYWRD 479
 QY 183 IKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAKSDEGHPP 242
 Db 480 IKKTGVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAKSDEGHPP 539
 QY 243 RAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFAVLMWVFTYVGA 302
 Db 540 RAYLESDVAVSEELQKYSNSVVLGHNGTVKELRRLFLVDDLVDSLKFAVLMWVFTYVGA 599
 QY 303 LFNGHTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIOAKIPGLKRAE 361
 Db 600 LFNGHTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIOAKIPGLKRAE 658

RESULT 15

Q7YRW9 PRELIMINARY; PRT; 199 AA.
 AC Q7YRW9;
 DT 01-OCT-2003 (TREMELrel. 25, Created)
 DT 01-MAR-2004 (TREMELrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
 DE RTN4-C.
 GN Name=RTN4;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactylia; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22715887; PubMed=12832288;
 RA Oertle T.; Klinger M.; Stuermer C.A.; Schwab M.E.;
 RT "A reticular rhapsody: phylogenetic evolution and nomenclature of the
 RT RTN/Nogo gene family."
 RL FASEB J. 17:1238-1247(2003).
 DR EMBL; AV164744; AAP47319.2; .
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
 DR InterPro; IPR003398; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 199 AA; 22395 NW; C60161DF3PB34D80 CRC64;

Query Match 50.1%; Score 927; DB 2; Length 199;
 Best Local Similarity 100.0%; Pred. No. 8e-23;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 174 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 233
 Db 12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOAI 71
 QY 234 QKSDEGHPPRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFAVL 293
 Db 72 QKSDEGHPPRAYLESEVAISELVQKYSNSALGHVNCITIKELRRLFLVDDLVDSLKFAVL 131
 QY 294 MWVFTVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIOAKI 353
 Db 132 MWVFTVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIOAKI 191
 QY 354 PGLKRAE 361
 Db 192 PGLKRAE 199